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1: gb_ba:*

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Match 99.6%; Score 1183; Local Similarity (100.0%; Pred. No.	AR012692 1188 bp Sequence 2 from patent US 5763589 AR012692.1 GI:3971010 Unknown. Unknown. Unclassified. 1 (bases 1 to 1188) 1 (bases 1 to 1188) 1 (bases 9 to 1018) 1 (bases 1 to 1188)	ALIGNMENTS	1183 99.6 1188 6 AR012692 11360 97.6 1303 9 AF190167 1135.2 95.3 1260 9 AF282596 1130.4 95.2 1244 9 AK027405 1130.4 95.2 1244 9 AK027405 1130.0 95.1 1262 9 BC014990 1120 94.3 1257 9 BC013025 867.4 73.0 1253 10 AF233178 851.6 71.7 1565 10 BC0030425 516.6 43.5 691 6 AX260945 315.6 23.0 740 6 AX260945 315.6 26.6 186556 2 AX269945 315.6 26.6 186556 2 AX2393706 240.2 220.7 1267 8 AX2939109 240.2 22.7 1267 8 AX293179 269.4 22.7 1267 8 AX293139 269.4 22.7 1267 8 AX293139 269.4 22.7 1267 8 AX293139 269.4 22.7 1267 8 AX293135 269.8 13.2 948 1 AX226511 269.8 13.1 948 1 AX226514 269.8 13.1 948 1 AX235154
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Identification and characterization of human homologue of stomatin (band 7.2b) present in
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97.6%; 99.4%;

1797656 segs, 10463268293 residues

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US-09-898-216-2

Perfect score:

Sequence:

Scoring table:

OM nucleic - nucleic search, using sw model

Total number of hits satisfying chosen parameters:

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Minimum DB seq Maximum DB seq

summaries

Post-processing: Listing first 45

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Database :

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150358 Sequence 6
170387 Sequence 6
18539 Sequence 6
18653 Sequence 6
18045 Sequence 4
19022 Sequence 1
104241 Sorangium C
AL035460 Human DNA
AC025033 Homo sapi
AC20915 Homo sapi
AC20915 Homo sapi
AC11003 Homo sapi
AC11003 Homo sapi
AC104027 Homo sapi
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AC094506 Rattus no
AR044578 Sequence
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(bases 1 to 1188)
Hillman, J.L. and Goli,S.K.
Human membrane protein
Patent: US 5763589-A 2 09-JUN-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1188;
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AR012692.1 GI:3971010
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AL391668
AX261093
A74641
A77620
A77620
AC09425
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ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
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13110.468 Million cell updates/sec
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1 GGCTTCTGGGAGCNACCGCT......GGAAGCAGATTTTCCTGATT 1188
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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SUMMARIES

Query Match Length DB

Score

Result ٠ 9

em_htg_inv:*
em_htg_other:*
em_htgo_inv:*

em_un:* em_vi:* em_htg_hum:*

em_ph: * em_pl: * em_ro: * em_sts: *

em_om: * em_or:* em_ov:*

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                                                                                                                                    GAGCCTGGTTTGAACATCCTCATCCCTGTGTTAGACCGGATCCGATATGTGCAGAGTCTC
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Conservative
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TVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzyninski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedl, Jacquellne Schelin, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott, George Yang, Scott Zuyderduyn, Marco Marra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (06-FBB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                             CAGGGTACAGATGCAAGTNTTGATGAGGAACTTGATCGAGTCAAGATGAGTTAGTGGAGC 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mall.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo
1 (bases 1 to 1257)
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/lab_host="DH108-R"
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/db_xref="LocusID:30968"
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complete cds.
BC003025
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Gaps

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Length 16; 0; Indels

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Ouery Match 2.0%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 5.8; Matches 7; Conservative 0; Mismatches
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Patent No. 5670483
GENERAL INFORMATION:
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HSA chromosome

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/product="stomatin-like protein 2"
/protein_id="AAF91466.1"
/protein_id="AAF91466.1"
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//translation="maraarsgralLilrgsilassrappraassglprntvvlevpogeawvvermgrehrilepglnilipvldriryvoslkeivinvpegsavtldnvtloid gyllylrindpyrasygvedperrayvolagoryrkeivinvpegsavtldnvtloid invaadowgirkasygvedperrayvolagoryrkeivinvpegsavtldnvthvprivesbydygvargrkrayvlesegtresalnva biskroholiasebarracinolaanseit tyvaegyvsafsklakdsvillipsnpsdpvtswvaqamgvygalitraadrophospaasit
Tvaegyvsafsklakdsstillepsnpsdpvtswvaqamgvygalitrappslessg
                             Homo sapiens stomatin-like protein 2 (SLP2) mRNA, complete cds. AF282596
AF282596 I GI:9652258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="member of the stomatin/band7/EpB72/MEC2 family; similar to the predicted Caenorhabditis elegans protein F:30Al0.5, to Caenorhabditis elegans MEC-2, and to the Homo
                                                                                                                                                                                                                                                                                                                                                      Submitted (26-JUN-2000) Monash Institute of Reproduction and Development, Monash University, Monash Medical Centre, 246 Clayton Road, Clayton, Victoria 3168, Australia Location/Qualifiers
                                                                                                                                                                                                Kola, I. and Hertzog, P.J.
A novel member of the STOMATIN/EPB72/mec-2 family, stomatin-like (STOML2), is ubiquitously expressed and localizes to HSA chromoso
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czarek, C.M., Treutlein, H.R., Portbury, K.J., Gulluyan, L.M.
                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Owczarek,C.M., Treutlein,H.R.,
Kola,I. and Hertzog,P.J.
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/note="member of the
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/dev_stage="fetus"
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/gene="SLP2"
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Strausberg, R. Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
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/translation="MLARAARGTGALLLRGSLLASGRAPRASSGLPRNTVVLFVPQQ
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GVLYLRIMDPYRAS(VGVEDPEYAYTQLAQYTMRSELGKISLDKVFRERESLNSIVDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAL Plate: 34 Row: p Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                      cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) MA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
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/tissue_type="Pancreas, epithelioid carcinoma"
/lab_host="NHH MCC_42"
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                                                                                      Project URL: http://mgc.nc1.nih.gov
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/db_xref-"GI:15929070"
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99.8%; Pred. No. 0;
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33. .1103
                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Location/Qualifiers
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PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-152-488-3
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Length 29; Query Match 2.0%; Score 7; DB 1 Best Local Similarity 100.0%; Pred. No. 9.8 Matches 7; Conservative 0; Mismatches

Gaps

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0; Indels

249 AKAKAKA 255 δλ QQ

GENERAL INPORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN AND
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
ITILE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 512 Springfield avenue
CITT: Cranford
STREET: New Jersey Sequence 3, Application US/08152488 Patent No. 5534619

STATE: New Jersey
COUNTRY: United States of America
ZIP: 07016-1811
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-D6
OPERATING SYSTEM: MS-D6
OPERATING SYSTEM: MS-D6
OPERATING SYSTEM: US-08/152,486
FILING DATE: 12 NOV-1993
CLASSIFICATION NUMBER: US-08/152,486
FILING DATE: 12 NOV-1993
CLASSIFICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATONNEY-AGENT INPORMATION:
NAME: ROAM, Benita J.

TELEFAX: 908-276-5533 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 29 amino acids

ORGANISM: N/A
UBLICATION INFORMATION:

TOPOLOGY: N/A MOLECULE TYPE: peptide ORIGINAL SOURCE: TYPE: amino acid STRANDEDNESS: N/

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clone MGC:1179 IMAGE:3346384, mRNA
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                                                                                         TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1278)
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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BC002442.1 GI:12803254
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KEYWORDS
SOURCE
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COMMENT
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov scries: IRAL Plates 5 Row: m Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9652258.
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GVIYLKINDPYKASYGVEDPEYAVQLAQTYMKSELGKLSLDKVFRERESLINSIVDA
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TVAEQYVSAFSKLAKDSNTILLPSNPGDVTSWVAQAMGVYGALTKAPVPGTPDSLSSG
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                                                                                                                                            Contact:
Shevofenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Shevofenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Boulfard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspl, R.,
Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MLARAARGTGALLLRGSLLASGRAPRRASSGLPRNTVVLFVPQQ
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland:
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Wang, Y. and Morrow, J.S.
Identification and characterization of human SLP-2, a novel
homologue of stomatin (band 7.2b) present in erythrocytes and other
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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Wang, Y. and Morrow, J.S.
Direct Submission
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/product-"membrane associated protein SLP-2"
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/translation-"mLaraarGTGALLLRGSLLASGRAPRRASSGLPRNTVVLFVPQO
EAWVERMERRHRILEPGINLIPPLDRIRYVQSLREIVINPEDSAYTLDNYTGID
GVLVLRIMDPYRASYGVEDPERAYTOLAGTTRRSELGKLSLDKPERERESLANSIVDA
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TVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSG
                    /note="stomatin-like protein 2; widely distributed perbipheral membrane protein; similar to human erythrocyte stomatin and MEC 1 of Caenorhabditis elegans; thought to be involved in mechanoreception or lipid domain
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Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mall:genomics@tri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, Fesearch Association for Biotechnology; CDNA library construction, Fesearch Institute (supported by Japan Key Technology Center etc.)
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1 Isogal, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shirratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T., Ninobilished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CACAACATAATGGAGATGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGT
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                                                                                                                                                                                                                                               and Department of Virology, Institute of Medical Science
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clone NT2RM1000080,
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Homo sapiens teratocarcinoma cell_line:NT2
clone_lib:NT2RM1 clone:NT2RM1000080
Homo sapiens
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/clone_lib="NT2RM1"
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Location/Qualifiers
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//tanslation="MLARARGTGALLLIRGSLLASGRAPRRASSGLPRNTVVLFVPQQ
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EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASL
TVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSG
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Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspl,R.,
Lim,M., Maduro,O.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="Miaraarctgalllrgsllasgraprrassglprntvvlevpoo
Eawwermgrehriedglatlipvldrirvvgslkeivinvpegsaytldnvtlotd
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Egkkqaqilasbabrabginopaagbasavlakakarafatllaaaltqhngdaaasl
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                                                                                                                                                                                                  p mRNA linear PRI 12-JUL-2001 clone MGC:19715 IMAGE:3534656, mRNA,
                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1281)
                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (02-UUL-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 27 Row: d Column: I that clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                951 CCAGCATGGTGGCTCAGGCCATGGTGTATATGGAGCCCTCACCAAAGCCCCCAGTGCCGG 1010
980 CCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTCACCAAAGCCCCAGTGCCAG 1039
                                                                    1040 GGACTCCAGACTCACTCTCCAGTGGGAGCAGCAGGAGATGTCCAGGGTACAGATGCAAGT 1098
                                                                                        Contact: MGC help desk
Email: ggapbs r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Galthersburg, Maryland;
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/db_xref="taxon:9606"
/clone="MGC:19715 IMAGE:3534656"
/clone_lib="Lung, small cell ca
/clone_lib="NHH_MGC_7"
/lab_host="DH10B-R"
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nisc_mgc@nhgri.nih.gov
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/protein_id="AAH10152.1"
/db_xref="GI:14603403"
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TVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSG
SSRDVQGTDASLDEELDRVKMS"
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                                                                                    Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (sites)

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Canaga: An and Secrist, H.

Compositions and methods for the therapy and diagnosis of colon cancer.
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100.0%; Pred. No. 2e-262;
iive 0; Mismatches 0
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AX193464
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                                                                                                                                                               Patent: WO 0196388-A 193 20-DEC-2001;
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                   Sequence 193 from Patent WO0196388. AX339946
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                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
123 c 137 g 73
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1. .457
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Magagher, M.J., Xu,J. and King,G.E.
Compositions and methods for therapy and diagnosis of colon cancer
Patent: WO 0173027-A 1428 04-OCT-2001;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 518)
Xu, J., Lodes, M.J., Secrist, H., Benson, D.R., Meagher, M.J., Stolk, J.A., King, G.E., Wang, T. and Jiang, Y.
Compounds for immunotherapy and diagnosis of colon cancer and methods for their use
Patent: WC 0149716-A 1031 12-JUL-2001;
CORIXA CORPORATION (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.5e-208;
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Sequence 1428 from Patent WO0173027.
AX261777
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/db_xref="taxon:9606"
136 c 149 g 109
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Matches 515; Conservative
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Best Local Similarity 99.5
Matches 219; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L.
Hepler, W.T.
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                                                                                                                       1; Indels
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                                                                                                Length
                                                      16
                                                                                                Score 331; DB 6; I
Pred. No. 5.5e-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.0%; Score 250; DB 6; 199.7%; Pred. No. 5.6e-139; iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
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                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 bp
Sequence 26 from Patent WO0179286.
AX302706
AX302706.1 GI:17383208
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                                                       140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
96 c 72 g 83
                      1. 691
/organism="Homo sapiens"
/db_xref="taxon:9606"
168 c 184 g 14(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
            Location/Qualifiers
                                                      184 g
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                                                                                                                                                                                                                                                                                                                                                                                                           560 ACTGCTGGGGTATCCGCTGCCT 581
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   CORIXA CORPORATION (US)
                                                                                                27.98;
99.78;
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10; Conservative
                                                                                                                       Conservative
                                                                                                             Similarity
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                                                                                                Query Match
Best Local S:
Matches 381
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DEFINITION
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ORIGIN
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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            FEATURES
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AC026501 55406 bp DNA 11near HTG 22-MAR-2000
Homo sapiens chromosome 1 clone RP11-266M12 map 1, LOW-PASS
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        PAT 26-OCT-2001
                                                                                                                                                                                                                                    cancer
                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 ATTGTCATCAACGTGCCTGAGCAGTCGGCTGTGACTCTCGACAATGTAACTCTGCAAATC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGGAGTCCTTTACCTGGGGATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGAC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTTTGAACATCCTCATCCTGTGTTAGACCGGATCCGATATGTGCAGAGTCTCAAGGAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTGTCATCAACGTGCCTGAGCAGTCGGCTGTGACTCTCGACAGTGTAACTCTGCAAATC 239
                                                                                                                                                                                                            Meagher, M.J., Xu,J. and King,G.E. Compositions and methods for therapy and diagnosis of colon Patent: WO 0173027-A 596 04-OCT-2001; CORIXA CORPORATION (US)
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          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 169; DB 6;
Pred. No. 5.8e-90;
0; Mismatches 1;
          DNA
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Sequence 596 from Patent W00173027.
                                                                                                                                                                                                                                                                                                                                                                            159
                                                                                                                                                                                                                                                                                                                 1. 740
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181 c 169 g 159
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                    AX260945.1 GI:16509912
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99.5%;
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AC026501/c
LOCUS
DEFINITION
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bp in length

SOURCE

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54 10363: gap of 100 bp 11053: contig of 690 bp in length 1153: gap of 100 bp 1153: gap of 100 bp 11848: contig of 695 bp in length 1948: gap of 100 bp 12539: gap of 100 bp 12539: gap of 100 bp 100 bp 12539: gap of 100 bp 13444: contig of 705 bp in length 1012739: gap of 100 bp 13444: contig of 705 bp in length
                                                                         100 bp
f 697 bp in length
                                                                                                                                                                                                                                                                                                                          100 bp
f 683 bp in length
                                                                                                                                                               100 bp
if 709 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    544: gap of 100 bp
14237: contig of 693 bp il
337: gap of 100 bp il
15047: contig of 710 bp il
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f 714 bp i
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10263: contig of 697 bp
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33270: contig of 711 bp
33370: gap of 100 bp
34172: contig of 702 bp
34172: gap of 100 bp
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contig of 694 bp
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20486: ~___36.
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15720: cont
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J: gap of
32459:
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gap of
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7869: cor
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9466: co
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7060: co
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Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Bouklagiter, B., Brown, A., Burkett, G.,
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Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Voung, G., Zainoun, J., Zimmer, A. and Zody, M.,
Direct Submission

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                                                                                                                                                                                                 Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 55406)
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
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677 776: gap of 100 bp
777 1478: contig of 702 bp in length
1479 1578: gap of 100 bp
1579 2267: contig of 689 bp in length
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f 685 bp in length
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f 718 bp in length
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                                                                                                                                                                                                                                                                                                                                                        Birchen, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 1, clone RP11-266M12 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This record contains 70 individual
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Project Information
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Center clone name: 266_M_12
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, u: gap of
, 1 4671: cort
? 4771: ap-
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3052: con
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3870: con
                                           AC026501
AC026501.1 GI:7283191
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Burkhart-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S., Phan, H., Velasco, N., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S., Christensen, M., Georgescu, A., Avlla, J., Liu, S., Attix, C., Andreise, T., Trankheim, M., Amico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Montgomery, M., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.O. and Carrano, A.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (25-MAR-1998) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Location/Qualifiers
                                                                                                                                                                                            Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence analysis of a human Pl clone containing the XRCC9 DNA repair gene Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Fibroblast or foreskin"
/lab_host="NS3316"
/note="Pl clone obtained from Genome Systems, Inc."
complement(4. .80)
sapiens chromosome 9, Pl clone 11659, complete sequence
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
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complement(7560. .8234)
/rpt_family="MER4A"
8239. .914
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complement(402. .626)
/rpt_family="MER4_internal"
complement(707. .1338)
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rpt_family="MER4_internal"
534. 5723
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/db_xref="taxon:9606"
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omplement(171)
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/rpt_family="HERVH"
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/rpt_family="MER83"
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/rpt_family="HERVH"
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/rpt_family="LTR7"
complement(5036. 5621)
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/clone="P1.11659"
/sex="Male"
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                                                             AC004472.1 GI:2984582
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Lamerdin, J.E.
                                                                                                                                                                                                                                                      (bases 1 to 86765)
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f 703 bp in length
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f 691 bp in length
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f 691 bp in length
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53822: contig of 704 bp in length
22: gap of 100 bp
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54717: gap of 100 bp
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685 bp in length
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683 bp in length
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50640: contig of 667 bp in length
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696 bp in length
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Pred. No. 7.6e-78;
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100.0%; Pred. No. ...
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4 45223: gap of 100
4 45928: conti
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35630: contig of
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36436 36535; gap of 1
36536 37220; contig of
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40347: contig of
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44335: contig of
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47524: contig of
34836: contig of
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49107:
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52222:
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46720: cont
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37983 38082; gap of
38083 38777; cont
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41129: con
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45123: cont
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53018: conf
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54617: con
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Best Local Similarity 100.
Matches 149; Conservative
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8239. .9165 /rpt_family="MSTB-internal" complement(9215. .9483)

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PRI 15-JUN-2001

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DNA

86765 bp

AC004472

RESULT 15 AC004472/c LOCUS

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/rpt_family=AtuJo.
/rpt_family=AtuJo.
/rpt_family=MIR"
.22765..2291
/note="predicted exon, program: grail2exons_human_1.3,
fincte="predicted exon, program: grail2exons_human_1.3,
fincte="predicted exon, program: grail2exons_human_1.3,
fincte="predicted exon, program: grail2exons_human_1.3,
fincte="predicted exon, program: grail2exons_human_1.3,
fincte="possimilarity: excellent, score: 86.000"
/rote="DDS similarity to A382319 EST95595 Testis I Homo
sapiens cDNA 5' end. Score: 505 Identity: 258/260 (99%)."
25318. 25897
//note="DDS similarity to AA061824 ml33d04.rl Stratagene
mouse testis (#93738) Mus musculus cDNA clone 513799 5';
Score: 279 Identity: 295/477 (67%).~(25480. 25887) BLASTN
similarity to AA866210 (1. 407); match: 1, score:
5.7e-157; database searched: month.na; ak48c12.sl Scares
restis NHT Homo sapiens cDNA clone IMAGE:1409206 3'"
/rote_family="MLTID"
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/note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: good, score: 50.000"
complement(29628...29915)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="Alusp"
complement'77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(27644, 27716)
/rpt_family="MLT1D"
27727, 28020
                                                                                                                                                                                                                                                                           complement(21324. .21361)
/rpt_family="MIR"
21365. .21487
                                                                                                                                                                                                    'rpt_family="LTR10C"
complement'>1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AluJb"
complement(26831. .27035)
/rpt_family="MLTID"
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/rpt_family="Aluy"
complement(27334. .27637)
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21491. .21793
/rpt_family="AluJb"
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18681. .28972
                                                                                                                                                                           /rpt_family="LINE2"
complement(20739.
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20258. .20313
                                       'rpt_family="Aluy"
9288. .20021
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//rpt_family="Alusg"

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                                   484. .9748
rpt_family="MSTB-internal"
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                                                                                                                                                                                                                             rpt_family="Alusg"
1777. .12076
                                                                                                                                                                       complement(10291. 10484)
/rpt_family="AluJo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(13041. .13531)
/rpt_family="LINE2"
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rpt_family="(TAAA)n"
2479. .12775
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16932. .16978
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4620. .14895
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2077. 1210s
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3945. 14247
rpt_family="Alusq"
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4504. 11610
/rpt_family="AluJo"
9484. .9748
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rpt_family="MSTB"
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Human; integral membrane protein; IMP; cancer; anaemia; prostate;
breast; pancreatic; tumour; ion transport; ss.
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/product= "integral membrane protein"
/transl_except= (pos:490..492,aa:Xaa)
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        version 4.5
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                                                 OM nucleic - nucleic search, using sw model
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AAX04345
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                                                                                                                                                                                               variety of tumours, e.g. haemolytic anaemias and prostate, breast and pancreatic tumours. A vector capable of expressing IMP, or a fragment or a derivative thereof, may also be administered to a subject to treat the haemolytic anaemias and prostate, breast and pancreatic tumours.
                                                                              DNA encoding human integral membrane protein - useful for producing recombinant protein, for treatment of anaemia and cancer
                                                                                                                                                     The present sequence encodes human integral membrane protein (IMP) IMP may be administered to a subject to treat disorders associated with abnormal ion transport or membrane conductance as well as a
                                                                                                                                                                                                                                                                        Sequence 1188 BP; 268 A; 316 C; 362 G; 237 T; 5 other;
                                                                                                                             Column 37-40; 33pp; English
                                       WPI; 1998-347418/30
                                                       P-PSDB; AAW57232
            SK,
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ö 420 480 009 900 099 720 240 300 300 360 360 420 GGCTTCTGGCCGCGCTCCGGCCGCGCCTCCTCGGATTGCCCCGGAAACACGGGGTACTG 180 180 Gaps AAACTCTCTNTGGACAAAGTCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGAT GCCATCAACCAAGCTGCTGACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGAT ATCCATGTGCCACCCCGGGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGG AAACGGGCCACAGTTCTAGAGTCTGAGGGGACCCGAGAGTCGGCCATCAATGTGGCAGAA caaatcgatggagtcctttacctgcgcatcatggacccttacaaggcaagctacggtgtg GAGGACCCTGAGTATGCCGTCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGC GGCTTCTGGGAGCNACCGCTCGCTCGTTCGTTGGTTCCGGAGGTCGCTGCGGCGGTGG GAAATGCTGGCGCGCGCGCGCGGGGCACTGGGGCCCTTTTGCTGÄGGGGCTCTCTACT gaaatgetggegegegegegeggggggaectgggggeecttttgetgaggggeteteact TTCGTGCCGCAGCAGGAGGCCTGGGTGGTGGAGCGAATGGGCCCGATTCCACCGGATCCTG GAGCCTGGTTTGAACATCCTCATCCTGTGTTAGACCGGATCCGATATGTGCAGAGTCTC CAAATCGATGGAGTCCTTTACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTG Length 1188; ; 0 0; Indels 19; DB 100.0%; Score 1188; 100.0%; Pred. No. 0; tive 0; Mismatches Conservative Similarity Best Local Sim Matches 1188; Match 541 601 601 61 121 121 181 181 241 241 301 301 361 361 421 421 481 481 541 Query g q δ g ò g ò g ö g ò Q δ g οy g ŏ ò a ò g õ

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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; ospitity edisorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                      TCCAACCCTGGCGATGTCACCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTC 1020
                                                                                                                                                                                                                                                                                             GAGCAGTATGTCAGCGCGTTCTCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCC
                                                                                                                                                     ACCAAAGCCCCAGTGCCAGGGACTCCAGTCTCTCCAGTGGGAGCAGCAGAGATGTC
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                                                GCAGCAGGAGGCCAGTGCAGTTCTGGCGAAGGCCAAGGCTAAAAGCTGAAGCTATTCGA
                                                                                             TGGGCTTNGCCAGGGAGTCTGGGGACAAGGAAGCAGATTTTCCTGATT 1188
                                                                                                                                                                                                                                                                                                                                          Human secreted protein gene 35 clone HTXCS21.
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Human; cytokine; cell proliferation; cell differentiation; growth factor haematopoiesis regulation; tissue growth; immunomodulator; activin; hinhibin; chemctaxis; chemokinesis; thrombolysis oncogenesis; proliferation: metastasis; cancer; tumour; haematopoietic disorder; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antinflammatory; antiatthmatic; antiarthitic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
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                                                             teacceagetageteaaacaaeceatgagateagageteggeaaaetetetetetggaeaaag
                                                                                          TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG
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                                                                                                                                                                                                                                   Human SLP-2 homologue-encoding cDNA, SEQ ID NO:1001.
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To protein as compared to the human protein only.

The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAX78126-W78225) which are useful for preventing, traating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypuciectides in a sample or by determining the presence of mutations in the new polymuclectides. Specific uses are described for each of the 86 polymuclectides, based on which tissues they are most highly expressed in
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Y, Young P
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                                                                                                                                                                                                                                                                                             P, Greene JM,
Ruben SM, Shi
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sen HS, Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 201-202; 380pp; English.
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           9705-0052989.
9705-0051919.
9705-0055984.
9705-0058665.
9705-0058668.
                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
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Olsen HS,
                                                                                                                                                                   97US-0060834.
                                                                                                                     97US-0058971.
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nes 957; Conservative
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                                        18-AUG-1997;
12-SEP-1997;
12-SEP-1997;
12-SEP-1997;
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12-SEP-1997;
12-SEP-1997;
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                              08-JUL-1997
                                                                                                        12-SEP-1997
                                                                                                                                                                                    02-OCT-1997
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Yu GL;
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Drmanac RT;
          05-FEB-2001; 2001WO-US03800.
               2000US-0496914
                  2000US-0560875
                                 2001-457740/49.
                       (HYSE-) HYSEQ INC
                             Tang YT, Liu C,
                                    P-PSDB; ABB11981
WO200157188-A2
               03-FEB-2000;
27-APR-2000;
     09-AUG-2001
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Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer

Claim 1; Page 851; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and conserved ABB10981-ABB12330 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides. Constitution days of producing the novel polypeptides of the invention. Although novel many of the undertient of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence controlled the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence controlled thereby giving an insight into their probable biological activities, and hence of interpretation activities, including cytokine, cell proliferation or cell manusmodulatory activity; tissue growth activity; mematopolesis regulatory activity; tissue growth activity; immunodulatory activity; tissue growth activity; immunodulatory activities; properties of more activities; content in their confidence of the invention are useful for perventing, treathed activities; or may be encoorgenesis, cancer cell proliferation or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include cancers, heamatopoletic disorders (e.g., myabloid or lymphoid cell of sorders) conditions, e.g., by protein or gene therapy. Such conditions include cancers, heamatopoletic disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair of bacterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal repair growth. Polypeptides involved with tissue regeneration and repair of propriet activities may be used to promote cell growth. Polypeptides may be used to promote cell growth. Factor activity may be used in cell cultures to promote cell growth. Factor activity may be used to promote cell growth. Factor activity may be used to promote cell growth. Factor activity may be used to supply be use

Sequence 1398 BP; 307 A; 408 C; 359 G; 324 T; 0 other;

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                                            GCCGCGCCTCCTCTGGATTGCCCCGGAAACACCGTGGTACTGTTCGTGCCGCAGCAGGAGG 199
                         Gaps
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 Length 1398;
                        Indels
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  DB 22;
Score 857; DB
Pred. No. 0;
0; Mismatches
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 72.1%;
99.8%;
                        Conservative
          al Similarity
957; Conserv
Query Match
Best Local Si
Matches 957,
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CCTGGGTGGTGGAGCGAATGGGCCGATTCCACCGGATCCTGGAGCCTGGTTTGAACATCC 259 200

Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.

1015 CCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTCACCAAAGCCCCAGTGCCAG 1039 1194 CTGGGTGGTGGAGCGAATGGGCCGATTCCACCGGATCCTGGAGCCTGGTTTGAACATCC 1135 439 895 619 775 199 859 AGTCTGAGGGGACCCGAGAGTCGGCCATCAATGTGGCAGAAAAGGGAAGAAAAACAGGCCCAGA 739 TCTCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCA 979 TCATCCCTGTGTTAGACCGGATCCGATATGTGCAGAGTCTCAAGGAAATTGTCATCAACG ACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGG TGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAG CACAACATAATGGAGATGCAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGT CCAGCATGGTGGCTCAGGCCATGGTGTATATGGAGCCCTCACCAAAGCCCCAGTGCCAG TGCCTGAGCAGTCGGCTGTGAGTCTCGACAATGTAACTCTGCAAATCGATGGAGTCCTTT ACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCG TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG AGTCTGAGGGGACCCGAGGAGTCGCCATCAATGTGGCAGAAGGGAAGAAACAGGCCCAGA TCCTGGCCTCCGAAGCAAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCCAGTG CAGTTCTGGCGAAGGCTAAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGA TCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCAAACTCTCTNTGGACAAAG GGACTCCAGACTCACTCTCCAGTGGGAGCAGCAGATGTCCCAGGGTACAGATGCAAGT Human polynucleotide SEQ ID NO 2212. BP. 260 1134 320 1074 380 1014 1040 954 200 894 560 834 620 774 680 714 740 654 800 594 860 534 920 474 980 414 g g . D q QΩ g δy δ ò ò δy q ò δý qq δy QQ 셤 ò QΩ ò q g ò g ò δ ð

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CCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTCACCAAAGCCCCAGTGCCAG 1039
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                                                                                                                 TGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAG
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                                 CAGTICIGGCGAAGGCCAAGGCIAAAGCIGAAGCITAITCGAATCCIGGCIGCAGCICIGA
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                                                        TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG
                                                                                                     ACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fertility; analgesic; pain; antigen; ss
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                                                                                                                                                                                                                                                                                                                                                                    The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine. cell proliferentiation or which may induce production of other cytokines in other cell populations. The polypeptides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
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                                                                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides with cytokine-like activities
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R, Wang
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ang J, Ren F, Chen
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                                                                                                                                                                                                                                                                                                                         useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 4572; 6221pp; English.
                                                                                                                                                2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0728422.
                                                                                                                                                                                                                                 Drmanac RT,
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99.8%;
                                                                              2001WO-US04098
                                                                                                                         2000US-0598075.
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Best Local Similarity 99.8
Matches 957; Conservative
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                                                                                                                                                                                                                               Liu C, D
Wang D,
Yang Y, W
                                                                                                                                                                                                          (HYSE-) HYSEQ INC
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                                 WO200157190-A2
                                                                                                                                                01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                             05-FEB-2001;
                                                                                                                         20-JUN-2000;
                                                                                                                 27-APR-2000;
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                                                                                                    03-FEB-2000;
                                                        09-AUG-2001
                                                                                                                                                                                                                               Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                       Xue AJ,
            Ношо
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ischaemia reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rhematoid arthritis; diabetes mellitus; asthma:
                                                                                                             Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
encoding novel human secretory protein, Seq ID No 34.
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The invention relates to novel isolated human secreted polypeptides (I) and polypeptides (II) are useful for treating and polypucleotides (II). (I) and (II) are useful for treating influry, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral calling vivo disease, and amyotrophic lateral activity, regulation of haematopoiesis and is useful for treatment of contraction of the manatopoiesis and is useful for treating myaeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia con lymphoid cell disorders, platelet disorders such as thrombocytopenia cuicers, for treating osteopromis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for disorders, or periodontal disease. Furthermore, (I) is also useful for disorders including severe combined immunodeficiency (SCID), betterial or funcal infertions and treatment of lung or liver fibrosis, functions immuno disorders and fibrodians and survived immunodeficiency (SCID), betterial or funcal infertions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (1) affects biorlythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAS44920-AAS45295 represent novel human secreted protein
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Wang 7
                                                                                                                                                                                                                                                                                                                                                                            Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment cancer, neurological, inflammatory, and autoimmune disorders -
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AJ,
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T, Zhang J,
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                                                                                      14-JUL-2000; 2000US-0616847.
19-SEP-2000; 2000US-0665363.
20-OCT-2000; 2000US-0693267.
                                          2000US-0574454.
2000US-0596193.
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Yang Y,
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19-MAY-2000;
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Zhao QA,
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                                                               Score 857; DB 22; Length 9098; Pred. No. 0;
                           2; Indels
             Pred. No. 0;
0; Mismatches
72.1%;
99.8%;
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BP. AAX04402 standard; DNA; 1322 (first entry) 13-APR-1999 AAX04402; و RESULT

Human secreted protein gene 35 clone HTXCS21.

Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue, cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obsetty; osteoclast; thywus; osteoporosis; arthitis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

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The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAX04311-X04410; amino acid sequences AAX04325) which are useful for preventing, treating or amplicating medical conditions can be diagnosed by determining the amount of the new polypueldes in sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in
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Y, Young P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encode
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en HS, Rosen CA, Ruben SM, Shi
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Ni J, Olsen HS,
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P-PSDB; AAW78217.
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           Homo sapiens
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Yu GL;
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Length 1322;

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                                        CGCGCCTCCTCTGGATTGCCCCGAAACACCGTGGTACTGTTCGTGCCGCAGCAGGAGGCC
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therapy;

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The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set
compliantses: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises at 3'-end sequence, where the
coligonucleotide which comprises at 15 nucleotides and the combination of
the 5'-end sequence 3'-end sequence 15 selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
contection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers are also useful for the
cDNAs easily without any specialised methods. AAH03616 to AAH13628 and
AAH13633 represent human aniho acid sequences; AAB92446 to
AAB95893 represent human aniho acid sequences; and AAH13632
crepresent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene
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Otsuki T;
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A, Naqai K
                                                       sequence SEQ ID NO:11009
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Sugiyama T, Wakama
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27-AUG-1999; 99JP-0300233.
11.3AN-2000. 2000JP-0118776.
22-MAY-2000: 2000JP-0188767.
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Ishii S
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Homo sapiens

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Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                       tcatccctgtgttagaccggatccgatatgtgcagagtctcaaggaaattgtcatcaacg
                                         TGCCTGAGCAGTCGGCTGTGACTCTCGACAATGTAACTCTGCAAATCGATGGAGTCCTTT
                                                                                   ACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCG
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E, Wang T,
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15-FEB-2000;
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                                                                                                                                                                                         Υ;
                                                                                                                                                                                                                                                                                                                                                                                                             treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
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Wang ZW;
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Ren F, Chen R,
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Zhang J, Ren F
T, Goodrich R;
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llarity 99.8%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                              Claim 1; Page 1135-1136; 6221pp; English.
                                                                                                                                                                                                                                                                           useful in diagnosis and gene therapy
                                                                                                                                                                                      Tang YT, Liu C, Drmanac RT,
Zhao QA, Wang D, Wang J, Zh:
Xue AJ, Yang Y, Wejhrman T,
                                                                    2000US -0496914.
2000US -0560875.
2000US -0598075.
2000US -0629325.
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les 893; Conserv
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27-APR-2000;
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                                                      TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stolk JA;
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immunogenic; gene therapy; vaccine; colonic cancer;
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20000S-0504629.
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20000S-0575251.
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                                                                                                          The present invention describes colon tumour associated proteins (I) and the present invention describes colon tumour associated protein (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by contractions or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the parients own production of them. Additionally, (II) may be used to complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may calso be used as antigons in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity.

Anti-(I) antibodies and antagonists may also be used to down regulate to TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents in the presence of TCAP expression and activity.

CAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents in the presence of TCAP expression and activity.

CAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents incomplement assay (ELISA). AAIZ460 to AAIZ9512 represent nucleaded and animo acid sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colon tumor associated proteins and nucleic acids useful for prevention, diagnosis and treatment of colonic cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 518 BP; 123 A; 136 C; 149 G; 109 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 365; DB 22;
Pred. No. 4.5e-169;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        680 AGTCTGAGGGGACCCGAGAGTCGGCCATCAATGTGGCA 717
                                                                    Claim 2; Page 415; 472pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.7%;
99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Matches 515; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been sisolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homology searches to identify the clone.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primers useful for synthesizing full length cDNA clones and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGAACAGATAAATCAGGCAGCAGGAGAGGCCAGTGCAGTTCTGGCGAAGGCCAAGGCTA 823
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Nagai K, Kojima S, Otsuki T, Ko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 566;
                                                                                                                                                                                                                                                                                                                                                                     Human; full length cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                                                                                                                                                                                                                 Human cDNA clone representative sequence, SEQ ID NO: 2385.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.2%; Score 335; DB 22; L larity 100.0%; Pred. No. 2.4e-154; Conservative 0; Mismatches 0;
Isogai
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                                                                                                                                                      AAK93925 standard; cDNA;
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nes 335; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        are useful for removing tumour cells from samples (e.g. blood) and for cancer treatment. The polynucleotides sequences are also useful in gene therapy. AAS57325-AAS58880 represent the cDNA sequences of the
ACACTATCCTACTGCCCTCCAACCCTGGCGATGTCACCAGCATGGTGGCTCAGGCCATGG 1003
                                                        Th present invention relates to the isolation of novel cDNA sequences encoding for at least an immunogenic portion of human colon tumour proteins. The sequences of the invention are useful in pharmaceutical compositions and vaccines for the prevention and treatment of cancers such as colon cancer. They are also useful for the diagnosis and monitoring of such cancers. Antibodies to the colon tumour proteins and antigen presenting cells that express polynucleotides encoding colon tumour proteins can be used to inhibit the development of cancers. Treels that react specifically with colon tumour proteins
                                                                                                                                                                                                                                                                                                                                       Human; colon tumour protein; colon cancer; gene therapy; cytostatic;
                                                                         GIGTATATGGAGCCCTCACCAAAGCCCCAGTGCCAGGGACTCCAGACTCACACTCCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention that encode for portions of human colon tumour proteins.
               New colon tumour proteins and related nucleic acid, useful for treatment, prevention, diagnosis and monitoring of cancer -
                                                                                                                                                                                                                                                                                                        cDNA #1428 encoding portion of a human colon tumour protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 691 BP; 183 A; 168 C; 184 G; 140 T; 16 other;
                                                                                                               Claim 4; Page 281; 299pp; English.
                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                    AAS58752 standard; cDNA; 691
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                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been clones. 830 cDNA molecules sequences of 5 - and 3 - ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length but any special methods. The present sequence is a full length but and contains the contains t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human cDNA of the invention.
Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation {}^{\circ}
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TGCCTGAGCAGTCGGCTGTGACTCTCGACAATGTAACTCTGCAAATCGATGGAGTCCTTT
                                                                                                                                                                                        ACCTGCGCATC.ATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCG
                                                                                                                                                                                                                                                                                                  TCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCAAACTCTCTNTGGACAAAG
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S, Otsuki T, Koga
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T, Nagai K, Kojima S,
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11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
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P-PSDB; AAM93862.
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Length 691;

Score 331; DB 23; Pred. No. 2.2e-152;

27.9%; 99.7%;

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Conservative

Query Match Best Local Similarity Matches 381; Conserv

200 CCTGGGTGGTGGAGGGAATGGGCCGATTCCACCGGATCCTGGAGCCTGGTTTGAACATCC 259

cctgggtggtggtggagcgaatgggccgattccaccggatcctggagcctggtttgaacatcc 60

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                                                                                                                                                                                                                                                                                                                                                                                                                             gctgaacagataaatcaggcagcaggagaggccagtgcagttctggcgaaggccaaggct 1408
                                                                                                                                                                                                                                                                  762
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specification, but was obtained in CD-ROM format directly from EPO
                                                                                                                                                                   583 CGTTATGAGATCAAGGATATCCATGTGCCACCCCGGGTGAAAGAGTTTGTGCAGGTGAG
                                                                                                                                                                                                                                              GTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAGAGTCTGAGGGGACCCGAGAGTCG
                                                                                                                                                                                                                                                                                                                      GCCATCAATGTGGCAGAAGGGAAGAACAGGCCCAGATCCTGGCCTCCGAAGCAGAAAAG
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                                                                                           Length 2064;
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                                    581 G; 498 T; 0 other;
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                                                                                             Score 285; DB 22;
Pred. No. 8.4e-130;
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                                                                                                                                0; Mismatches
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                                        Sequence 2064 BP; 479 A; 506 C;
                                                                                             24.0%; {
100.0%;
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2000US-0192099.
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2000US-0205230.
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                                                                                           Query Match 24.0
Best Local Similarity 100.
Matches 285; Conservative
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14-MAR-2000;
24-MAR-2000;
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15-MAY-2000;
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detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                    776 ATCAGGCAGCAGGAGAGGCCAGTGCAGTTCTGGCGAAGGCCAAGGCTAAAGCTGAAGCTA 835
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                                                                                                                                              Length 313;
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                                                                                            Sequence 313 BP; 60 A; 86 C; 89 G; 78 T; 0 other;
                                                                                                                                            Score 253; DB 22;
Pred. No. 4.6e-114;
0; Mismatches 1;
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breast ca
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ID AAS46972 standard; cDNA; 301
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llarity 99.7%;
Conservative (
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08-JUN-2000; 2000US-0590751.
22-JUN-2000; 2000US-0604287.
20-JUL-2000; 2000US-0620405.
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Best Local Similarity
Matches 303; Conserv
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of

treatment and diagnosis of least an immunogenic portion

polypeptide useful for the breast cancer comprises at

Claim 6; Page 95; 238pp; English.

a breast tumor protein .

Harlocker

J,

хп

Mitcham JL,

Dillon DC,

Yuqiu J,

WPI; 2001-122627/13

An isolated e.g.

tumors

(CORI-) CORIXA CORP

99US-0285480. 99US-0339338. 99US-0389681. 99US-0433826.

02-APR-1999; 23-JUN-1999; 02-SEP-1999; 03-NOV-1999;

The present invention provides the coding sequences and some protein sequences of proteins associated with breast cancer in humans. These sequences can be used in the diagnosis and treatment of cancers,

Sequence 301 BP; 48 A; 96 C; 72 G; 85 T; 0 other;

particularly breast tumours.

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The invention relates to isolated breast tumour proteins and nucleic acids that encode them, including immunogenic fragments of the proteins. Also included are expression vectors expressing the proteins. Least including immunogenic fragments of transformed cells and antibodies raised against the proteins or proteins, transformed cells and antibodies raised against the proteins or uncleic acids may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate breast tumour protein expression, i.e. breast tumours and breast cancer e.g by gene therapy. The nucleic acids and their complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The proteins, nucleic acids and antibodies may be used in assays to identify modulators (e.g. antagonists) of breast tumour protein capteression and activity. The antibodies and antagonists may also be used to down regulate expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to as diagnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immuno-purification diagnostic techniques. The present sequence is a cDNA from a breast tumour formal breast tumour formal breast the present sequence is the protein and activity the acid the present sequence is the print of the present sequence is the protein and activity the acid that are accounted to the present sequence is the present accounted to the present accounted 
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Pred. No. 1.4e-112;
0; Mismatches 1;
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99.7%;
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Best Local Similarity 99.77
Watches 300; Conservative
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                                                                            301 AGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAGAGTCTG 242
                                                                                                       AGGGGACCCGAGAGTCGGCCATCAATGTGGCAGAAGGGAAGAAAAAAGGCCCAGATCCTGG 745
                                                                                                                                                         CCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCCAGTGCAGTTC 805
                                                                                                                                                                       TGGCGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACACAAC 865
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  Length 301;
                           Indels
Score 250; DB 22;
Pred. No. 1.4e-112;
0; Mismatches 1;
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Job time: 4267 sec
 21.0%;
99.7%;
Query Match
Best Local Similarity 99.7'
Matches 300; Conservative
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Human; breast cancer associated gene; vaccine; diagnosis; therapy; ss.

15-FEB-2000; 2000WO-US05308

WO200060076-A2 Homo sapiens

12-OCT-2000.

Human breast cancer associated JBTT21 coding sequence.

(first entry)

13-MAR-2001

AAF17542;

AAF17542 standard; cDNA; 301 BP.

AAF17542/C

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IMMEDIATE SOURCE:
LIBRARY: Consensus
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LIBRARY: Conservation
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Best Local Similarity
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1 GGCTTCTGGGAGCNACCGCT......GGAAGCAGATTTTCCTGATT 1188
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Pcxfiles1.seq:*
                                Compugen Ltd
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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US-08-457-6468-6
US-08-76-233A-4
US-08-729-214-6
US-09-028-934-6
US-08-333A-1
US-08-343-443B-1
US-08-343-443B-1
US-08-343-42B-34
US-08-29-665A-34
PCT-US-95-10398-34
US-08-29-665A-34
PCT-US-95-10398-34
US-08-29-665A-34
PCT-US-95-10398-34
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PCT-US-95-10398-34
US-08-29-665A-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-258-261B-6
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383533 seqs, 122816752 residues
                                                                                                                                                                      September 22, 2002, 15:26:33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Listing first 45 summaries
                                                                                                                nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                    US-09-898-216-2
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Match Length DB
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Sequence:
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                                                                                                              OM nucleic
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Sequence II, Appl
Sequence II, Appl
Sequence II, Appl
Sequence 26, Appl
Sequence 32, Appl
Sequence 124, Appl
Sequence 124, Appl
Sequence 19, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 7, Appli
                Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08781562

Patent No. 5763589

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Forter Drive
CITY: Palo Alto
STATE: CA.
US-08-480-547A-11

US-08-63-949A-11

US-08-464-410A-11

US-08-76-259-26

US-08-91-259-26

US-08-914-095-7

US-08-914-095-7

US-08-914-095-7

US-08-914-095-7

US-08-918-112-19

US-08-918-112-19

US-08-918-111-19

US-08-017-52A-1

US-08-017-52A-1

US-08-017-52A-1

US-08-017-52A-1

US-08-017-52A-1

US-08-017-52A-1

US-08-017-52A-1

US-08-017-52A-1

US-08-017-52A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastESC for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/781,562
                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF-0181 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKIST NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1188 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette
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STRANDEDNESS: single
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876
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MEDIUM TYPE: Diskett
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Length 1188;

DB 1;

Score 1188; Pred. No. 0;

100.0%; 100.0%;

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OPERATING SYSTEM:
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Best Local Similarity
Matches 21; Conserv
                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                      STATE:
                                                                                                        ; Patent No.
                                                                                                                                                                                                                                               CITY:
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                                               GAAATGCTGGCGCGCGCGCGCGCGGGGCACTGGGGCCCTTTTGCTGAGGGGCTCTCTACT 120
Gaps
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                       AAGGAAATTGTCATCAACGTGCCTGAGCAGTCGGCTGTGACTCTCGACAATGTAACTCTG
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                                                                               GGCTTCTGGCCGCGCGCCGCGCCCTCCTCGATTGCCCCGGAAACACGCGTACTG
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Mismatches
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Conservative
Matches 1188;
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CAGGGTACAGATGCAAGTNTTGATGAGGAACTTGATCGAGTCAAGATGAGTTAGTGGAGC 1140
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                                                                               APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Hammer, Phillip E.
APPLICANT: OF INVENTION: Genes for the synthesis of TITLE OF INVENTION: antipathogenic substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
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0.46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GGC 1506/CIP3
TELECOMUNICATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995 .
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,261
FILING DATE: 08-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: Floppy disk
IBM PC compatible
:YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                        Sequence 6, Application US/08258261B Patent No. 5639949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23859 GCGGGGTCCGGCCGCCTC 23879
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Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERISTICS:
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Length 28958;
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          APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Hammer, Phillip E.
APPLICANT: Genes for the synthesis of TITLE OF INVENTION: Genes for the synthesis of TITLE OF INVENTION: antipathogenic substances NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                             SCENAIRE: Patentin Release #1.0, Version #1.25 SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
. 0.46;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/457,342
FILING DATE: 01-UNN-1995
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-UN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 018-Unn-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REGISTRATION NUMBER: 36,129
REGISTRATION NUMBER: 36,129
REGISTRATION NUMBER: 36,129
REGISTRATION NUMBER: GGC 1506/CI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                          ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schupp, Thomas
Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
Gaffney, Thomas Deane
                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-457-646A-6
; Sequence 6, Application US/08457646A
; Patent No. 5679560
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100.08; Pre
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Hammer, Phillip E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 28958 base pairs
TYPE: nucleic acid
Ligon, James M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.8°
Best Local Similarity 100.
Matches 21; Conservative
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MEDIUM TYPE: Floppy
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APPLICANT: Schupp
                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ANTI-SENSE: NO US-08-457-342-6
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                                                                                                                                                                                                                                                                                                                                               10532
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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REDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,837
FILING DATE: 01-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/457,205
FILING DATE: 01-JUN-1994
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Eliner, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GC 1506/CIP3
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SED ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENTYH: 28958 base pairs
TYPE: UNCLEIC acid
STRANDEDNESS: single
                         APPLICANT: Schupp, Thomas

APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Hill, Dwight Steven
APPLICANT: Hill, Dwight Steven
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Hammer, Phillip E.
APPLICANT: Mones, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.46;
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Patent No. 5662898
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 23859 GCCGCGCTCCGGCCGCCTC 23879
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MOLECULE TYPE: DNA (genomic)
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US-08-456-837-6
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APPLICANT: Ligon, James M.
APPLICANT: Beck, James J.
APPLICANT: Beck, James J.
APPLICANT: Hill, Dwight S.
APPLICANT: Hill, Dwight S.
APPLICANT: Hill, Dwight S.
APPLICANT: Ryals, John M.
TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STREET: Tarrytown
STATE: W.
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                                                                                                                                                                              OPERATING SYSTEM: PC_LUDS,RD-LUDS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,076A
FILLING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
TELECOMMUNICATION INFORMATION:
TELECHOME: 919-541-8614
INFORMATION ESQ ID NO: 6:
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APPLICATION NUMBER: US/08/764,233A
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Pred. No. 0.46;
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                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 21; Conservat
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APPLICANT: Ligon,
     Hawthorne
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                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE:
US-08-458-076A-6
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                                                     COUNTRY:
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Pred. No. 0.46;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,646A
FILING DATE: 01-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ELHER, James Scott
RECIETRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GGC 1506/CIP3
TELEPAN: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                 TITLE OF INVENTION: Genes for the synthesis of TITLE OF INVENTION: antipathogenic substances NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS: ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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7 Skyline Drive
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Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
Gaffney, Thomas Deane
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Uknes, Scott Joseph
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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APPLICANT: Schupp,
                                                                                                                                                                       CITY.
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE:
US-08-457-646A-6
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US-08-458-076A-6
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Gaps
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Sequence 6, Application US/08729214
Fatent No. 5817502
GENERAL INFORMATION:
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Hammer, Phillip E.
APPLICANT: Wan Pee, Karl-Heinz
APPLICANT: Wan Pee, Karl-Heinz
APPLICANT: Wan Pee, Karl-Heinz
APPLICANT: Winner, Sabine
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,214
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. 0.46;
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                                   FILING DATE: 08-Jun-1994
TATORNEY, AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
TEFERENCE, DOCKET NUMBER: GGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGC 1506/CIP5
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100.0%; Pre
0;
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REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR CERV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSE: Ciba-Gengy Corrections Road CITY: Tarrytown
                      08/258,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 23859 GCGGGGTCCGGCCGCGCTC 23879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 GCCGCGCTCCGGCCGCCTC 149
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                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                  TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                  LENGTH: 28958 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                              single
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MEDIUM TYPE: Floppy
                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                 linear
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: D
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10591
                                                                                                                                                                                                                                                                                                                                                                               ; ANTI-SENSE:
US-08-457-335A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 28958;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Schupp, Thomas
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Ligon, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Hammer, Phillip E.
APPLICANT: Wenes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.8%; Score 21; DB 1;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 21; Conservative 0; Mismatches
             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILLING DATE: 09-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
FILLING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 1806/CIP6
TELEPONMUNICATION INFORMATION:
TELEPHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERESTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,335A
FILING DATE: 01-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Sorangium cellulosum
IMMEDIATE SOURCE:
CLONE: p98/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08457335A Patent No. 5723759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 23859 GCGGGGTCCGGCCGCCTC 23879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 GCCGCGCTCCGGCCGCCTC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                       FOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hawth
STATE: NY
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-457-335A-6
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Gaps

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Indels

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Pred. No. 0.46;
                                        Mismatches
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100.0%; Pr
                                                                                                                     Db 23859 GCGGGGTCCGGCCGCGCTC 23879
                                                                             129 GCGGGGCTCGGGCGGCGTC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Soranglum cellul
                                                                                                                                                                                                                                                                                                    APPLICANT: Schupp, Thomas APPLICANT: Beck, James J. APPLICANT: H111, Dwight S. APPLICANT: Neff, Snezanna APPLICANT: Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: 383..760
                  Best Local Similarity 100.
Matches 21; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GENUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 520 Whis
CITY: Tarrytown
STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                      US-08-764-233A-1
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                                                                                                                                                                                                            Gaps
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APPLICANT: Hill, Dwight S.
APPLICANT: Hill, Dwight S.
APPLICANT: Hill, Dwight S.
APPLICANT: Hammer, Philip E.
APPLICANT: Nan Pee, Karl-Heinz
APPLICANT: Nan Pee, Karl-Heinz
APPLICANT: Noung, Thomas R.
TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117670artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                          ;
0
                                                                                                                                                                  1.8%; Score 21; DB 1; Length 28958;
100.0%; Pred. No. 0.46;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,934
                                                                                                                                                                                100.0%; Preα. ...
+'ve 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILING DATE: 09-CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
FILING DATE: 08-UN-1994
ATTORNEY AGENT INFORMATION:
NAME: Meigs, J. TIMOTHY
REGISTATION NUMBER: 38,241
                                                                                                                                                                                                                                                                           Db 23859 GCGGGCTCCGGCCGCGCTC 23879
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09028934; Patent No. 6117670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
^~wpiffeR: IBM PC compatible
^~~nonfifeR: IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                      129 GCCGCGCTCCGGCCGCCTC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 28958 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                  DNA (genomic)
                                                                                                                                                                                       Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 GEGERAL INFORMATION:
APPLICANT: Ligon, J
APPLICANT: Hill, D
APPLICANT: Lam, Ste
APPLICANT: Hammer,
APPLICANT: Van Pee,
APPLICANT: Van Pee,
APPLICANT: You Pee,
                               linear
                         TOPOLOGY: lines MOLECULE TYPE: DN HYPOTHETICAL: NO
                                                                                    , ANTI-SENSE: NO
US-08-729-214-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE:
US-09-028-934-6
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                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-09-028-934-6
                                                                                                                                                                        Query Match
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Length 28958;

1.8%; Score 21; DB 3;

Query Match

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NAME/KEY: misc_feature
LOCATION: 927..19874
OTHER INFORMATION: /hote= "SorA"
OTHER INFORMATION: /hote= "Gene product is highly homologous to type I PKSs t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product- "SorR"

Anote- "This gene encodes a protein that is highly homolog the reductase domains of type I PKSs such as eryA from Saccharopolyspora erythraea."
Genes For The Biosynthesis Of Soraphen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,233A
                                                                                                                 ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILING DATE: 09-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Med49s. J. Timochy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 38,241
REFERENCE/POCKET NUMBER: 38,06/CIP6
TELEFOAMUNICATION INFORMATION: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 49377 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Sorangium cellulosum
IMMEDIATE SOURCE:
CLONE: p98/l, pJL3, and pVKM15
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CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
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Patent No. 5670317
GENERAL INFORMATION:
APPLICANT: Landanyi, Marc
APPLICANT: Gerald, William
TITLE OF INVENTION: A DIAGNOSTIC TEST FOR THE DESMOPLASTIC
TITLE OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION: 514
PRIOR APPLICATION DATA
APPLICATION NUMBER: PCT/FR93/00494
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/06123
FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989.6121P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18;
                                                                                                                                                                                                                                        ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                     E: Weiser & Associates
230 South Fifteenth Street
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/343,443B FILING DATE: 18-NOV-1994
                                                                   TRANSLOCATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08; FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 AGGAGGCCTGGGTGGTGG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2371 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: Z15 CT TELEPHONE: Z15-875-8394
                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York COUNTRY: U.S.A. ZIP: 10036 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
25..1992
                                                                                                                                                STREET: 230 com
      TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
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US-08-437-027-18/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION:
US-08-343-443B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1987I..46318
OTHER INFORMATION: /product= "SorB"
OTHER INFORMATION: /note= "dene product is highly homologous to type I PKS genes
OTHER INFORMATION: are known to be involved in the synthesis of polyketide OTHER INFORMATION: compounds."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "The protein encoded by the sorM gene is highly homologous to the methyltransferase from Streptomyces hygroscopicus that is involved in the synthesis of the polyketide rappamicin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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/ENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 21; DB 1; Length 49377; ilarity 100.0%; Pred. No. 0.46; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                 NAME/KEY: misc_feature
LOCATION: 942..7115
OTHER INFORMATION: /product= "Module 1 of Sora"
                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 13455..19616
OTHER INFORMATION: /product= "Module 3 of Sora"
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 19870..24556
OTHER INFORMATION: /product= "Module 1 of SorB'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 24638..30820
OTHER INFORMATION: /product= "Module 2 of Sorb'
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEX: misc_feature
LOCATION: 40190..46318
OTHER INFORMATION: /Product= "Module 5 of SorB"
                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 7203..12884
OTHER INFORMATION: /product= "Module 2 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 30881..35446
OTHER INFORMATION: /product= "Module 3 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 35528..40114
OTHER INFORMATION: /product- "Module 4 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 46651..47891
OTHER INFORMATION: /product= "Sorm"
OTHER INFORMATION: /note= "The prote
OTHER INFORMATION: homologous to the
OTHER INFORMATION: hygroscopicus the
OTHER INFORMATION: hygroscopicus tha
US-08-764-233a-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Delattre, Olivier
APPLICANT: Desmaze, Chantal
APPLICANT: Melot, Thomas
APPLICANT: Peter, Martine
APPLICANT: Ploougastel, Beatrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08343443B
Patent No. 5968734
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Best Local Similarity
Matches 21; Conserv
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APPLICANT: Aurias,
APPLICANT: Delati
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US-08-343-443B-1/C
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                                                                                                                                                                                                                                                                                                                                                 Length 576;
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MBER: 2026-4070US1
ORMATION:
58-4800
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APPLICATION NUMBER 19/08/468,570
FILING DATE: 6-JUN 1995
CLASSIFICATION: 42%
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APPLICATION NUMBER: 08/086,428
FILING DATE: 29-00N-1993
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
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TELECOMMUNICATION INFORMATI
TELEPHONE: (212), 758-480
TELEFAX: (212), 751$ 6849
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INDIVIDUAL ISOLATE
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; INDIVIDUAL ISOLATE:
US-08-086-428B-34
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Best Local Similarity
Matches 17; Conservat
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                                                                TYPE: nucleic acid
STRANDEDNESS: sing
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INFORMATION FOR SEQ ID
SEQUENCE CHARACTERIST
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TYPE: nucleic act
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ANINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF 51 ISOLATES OF HEPATITIS C AND THE USE
OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
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                                                                                       OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,027
FILING DATE:
CLASSIFICATION: 536
ATONNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERRACE/DOCKET NUMBER: 46416/JPW/CCA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 212-391-0525
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Mismatches
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FILING DATE: 29-JUN-1993
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345 PARK AVENUE
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COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MSPERM: PC-DOS/MSPERM: PATER-1
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OPERATING SYSTEM: PC-DOS/MS:
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
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ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
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Best Local Similarity 100.
Matches 18; Conservative
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TITLE OF INVENTION: DAIN
TITLE OF INVENTION: OF R
TITLE OF INVENTION: OF R
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Comportium (LLNL)
DNA Sequencing by: Agencourt Bioscience Comporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNM at:
http://image.llnl.gov
Plate: LLAM12233 row: a column: 09
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AGENCOURT_6465267 NIH_MGC_72
5', mRNA sequence
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 1037)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                      Unpublished (1999)
Contact: Robert Strausberg,
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EST.
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/clone_lib="NIH_MGC_72"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Site_2: Sall; Cloned unidirectionally. Primer: Average insert size 2 kb. Library constructed Technologies."
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Search completed: September 22, 2002, 16:48:50 Job time: 5157 sec

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602326409F1 NIH_MGC_91 Homo:
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D
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NIH-MGC http://mgc.nci.nih.gov/.
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:427787"
/clone_lib="NHL_MGC_91"
/tissue_type="adenocarcinoma, cell line"
/tab_host="DH10B (phage-resistant)"
/note="organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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National Institutes of Health, M
Unpublished (1999)
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Tissue Procurement: ATCC
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1 (bases 1 to 770)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                        /clone_lib="NIME_1495945"
/clone_lib="NIME_1495945"
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Query Match Best Local Similarity

> 45.48; 99.78;

Score Pred.

539; DB 10; No. 1.1e-260;

Length 770;

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KEYWORDS
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  Email:
Tissue
                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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603083364F1 NIH_MGC_120
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
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Plate: LLAM11559 row: p column: 16
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: pooled pancreas and spleen; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
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/clone_lib="NIH_MGC_120"
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/db_xref="taxon:9606"
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                                                                            CAGTTCTGGCGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGA
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                                        CACA 863
                          ATTGTGGATGCCATCAACCAAGCTGCTGACTGCTGGGGTATCCGCTGCCTCCGTTATGAG
                                                                                                                                                                                                                                                 668;
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CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11025 row: i column: 06
High quality sequence stop: 793.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                /note-"Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.5 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                                              Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:4997837"
/clone_lib="NIH_MGC_10"
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                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
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Pred. No. 2.5e-275;
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BE740453
BE740453.1 GI:
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1 (bases 1 to 660)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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601595494F1 NIH_MGC_9 Homo
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
Plate: LLCM814 row: k column: 23
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/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma cell line"
/tlab_host="pHIOB (phage_resistant)"
/note="organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCAGGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3949582"
/clone_lib="NIH_MGC_9"
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                                                                                                                                                      AGENCOURT_6479118
5', mRNA sequence.
BM476304
                                 Unpublished (1999)
Contact: Robert Strausberg,
                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1110)
           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                  1 (bases 1 to 1110)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Pred. No. 2.5e-277;
0; Mismatches 2;
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Plate: LLAM12282 row: k column:
High quality sequence start: 8
High quality sequence stop: 678.
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/clone_type="doublenal adenocarcinoma, cell line"
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AGENCOURT_6423435 NIH_MGC_67
5', mRNA sequence.
BM461614
BM461614.1 GI:18510654
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1011)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 622.
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/db_xref="taxon:9606"
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/clone_lib="NH_MGC_67"
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/tissue_type="retinoblastoma"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Si
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603623541F1 NIH_MGC_40 Homo sapiens
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Tissue Procurement: DCTD/DTP
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                           237
                                                       /tissue_type="carcinoma, cell line"
/lab_host="PH10B (phage-resistant)"
/note="Organ: prostate; vector: poTB7; Site_1: XhoI;
/note="Organ: prostate; vector: poTB7; Site_1: XhoI;
/note="Organ: prostate; vector: poTB7; Site_1: XhoI;
/note="Collaboration of the potential"
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/clone="IMAGE:5449259"
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                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1053)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collect Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5583626"
/clone_lib="NIH_MGC_92"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.78;
99.78;
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2.4e-280;
hes 2;
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DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM12347 row: a column: 03
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pcMv-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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1018

958 480 898 420 838 360 778 300 718

BM453159

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hes 752; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                    GAGATCAGAGCTCGGCAAACTCTCTNTGGACAAAGTCTTCCGGGAACGGGAGTCCCTGAA 524
                                                                                                                                                                                                                                                                                                                                  CATCAATGTGGCAGAAGGGAAGAAACAGGCCCAGATCCTGGCCTCCGAAGCAGAAAAGGC 764
                                                                                 GGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAGAGTCTGAGGGGACCCGAGAGTCGGC
                                                                                                                                              TTATGAGATCAAGGATATCCATGTGCCACCCCGGGTGAAAGAGTCTATGCAGATGCAGGT 644
                                                                                                                                                                                                  TGCCAGCATTGTGGATGCCATCAACCAAGCTGCTGACTGCTGGGGGTATCCGCTGCCTCCG
                                                                                                                                                                                                                   TGCCAGCATTGTGGATGCCATCAACCAAGCTGCTGACTGCTGGGGTATCCGCTGCCTNCG
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                                                                GGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAGAGTCTGAGGGGGACCCGAGAGTCGGC
                                                                                                                                  TTATGAGATCAAGGATATCCATGTGCCACCCCGGGTGAAAGAGTCTATGCAGATGCAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM12208 row: m column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BM453159
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National Institutes of Health, Mammalian
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:5529785"
/clone="tib="NH_MGC_71"
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/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1:
Site_2: Sali; Cloned unidirectionally. Primer: Oli
average insert size 2.1 kb. "
space 279 g 225 t
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99.7%;
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Primates;
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Pred. No. 0;
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AGENCOURT_6402181 NIH_MGC_41
5', mRNA sequence.
BM423347
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2017 row: b column: 20
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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                            285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 503.
                         Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

282 c 302 g 226 t
                                                                                                                                             /tissue_type="amelanotic melanoma, cell line"
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/lab_host="bH10B (phage=resistant)"
/note="0rgan: skin; Vector: poTB7; Site_1: xhoI; Site_2:
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/clone_lib="NIH_MGC_41"
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MAGE:5516467
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Prime, mRNA sequence.
AL525168 GI:12788661
                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 849)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
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segref@genoscope.cns.fr, V
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CSODC005YF20"
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/tissue_type="neuroblastoma
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was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and Eco RV sites of the pCMYSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
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KAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLA
KDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASLDE
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Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.ge
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TGGAGTCCTTTACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCC
                 TGGAGTCCTTTACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCC
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/lab_host="DH10B"
/note="Organ: placenta; Vector: pcMVSPORT 6; 1st strand
/note="organ: placenta; vector: Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pcMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact: Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
filang@lifetech.com URL:
http://fulllength.invitrogen.com"
4 others
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                               58.3%;
99.6%;
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Submitted (23-JUN-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II, Shanghai 200025, P.R. China Location/Qualifiers
1. .1218
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Zhang,Q.H., Ye,M., Wu,X.Y., Ren,S.X., Zhao,M., Zhao,C.J., Fu,G., Shen,Y., Fan,H.Y., Lu,G., Zhong,M., Xu,X.R., Han,Z.G., Zhang,J.W., Tao,J., Huang,Q.H., Zhou,J., Hu,G.X., Gu,J., Chen,S.J. and Chen,Z. Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells
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2 (bases 1 to 1218)
Ye,M., Zhang,Q.H., Zhou,J., Shen,Y., Wu,X.Y., Guan,Z.Q., Wang,L., Ye,M., Mao,Y.F., Dal,M., Huang,Q.H., Chen,S.J. and Chen,Z. Human full length cDNA cloned from cd34+ stem cells
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/db_xref="taxon:9606"
/clone="CBCAPB12"
/cell_type="cd34+ stem cells"
/tissue_type="blood"
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BM459766
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APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Chenault, Ruth A.

APPLICANT: Chenault, Ruth A.

APPLICANT: Chenault, Ruth A.

APPLICANT: Chenault, Ruth A.

APPLICANT: Meagher, Madelein Joy

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.561PC

CURRENT APPLICATION NUMBER: PCT/US01/43704

CURRENT FILING DATE: 2001-11-19

NUMBER OF SEQ ID NOS: 2606

SOFTWARE: COTIXA INVENTION DISCLOSURE DATABBASE

SEQ ID NO 58

LENGTH: 563

TYPE: DNA

ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                            Sequence 58, Application PC/TUS0143704 GENERAL INFORMATION:
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SEQ ID NO 841
LENGTH: 504
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                                                    tcttccgggaacgggagtccctgaatgccagcattgtggatgccatcaaccaagctgctg
                                                                TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG
                                                                                                     TCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCAAACTCTCTNTGGACAAAG
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Search completed: September 22, 2002, 18:19:49
Job time: 5451 sec

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GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Secrist, John A.
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANC
FILE REFERENCE: 210121.527C2
CURRENT APPLICATION NUMBER: US/10/146.502
CURRENT APPLICATION NUMBER: US/241
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 193
LENGTH: 454
TYPE: DNA
ORGANISM: Homo sapiens
US-10-146-502-193
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Best Local S
Matches 454
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                                            APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Smith, Carole L.
                                                                                                                                APPLICANT:
                                                                                                                                                                  APPLICANT: Jiang, Yuqiu APPLICANT: Chenault, Ru
TITLE
                            APPLICANT:
              APPLICANT:
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            Durham, Margarita Stolk, John A.
                                                                                                                                  Indirias, Carol Yoseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.2%; Score 454; DB 7; llarity 100.0%; Pred. No. 7e-224; Conservative 0; Mismatches 0
                                                                                                                                                Jiangchun
COMPOSITIONS
                                                                                                                                                                    Ruth A.
AND
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METHODS
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FITLE OF INVENTION: AND DIAGNOSIS OF COLON
FILE REFERENCE: 210121.563C1
CURRENT APPLICATION NUMBER: US/10/214,403
CURRENT FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 3420
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2995
LENGTH: 550
TYPE: DNA
ORGANISM: Homo saplens
APPLICANT: CORIXA CORPORATION
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Chemault, Ruth A.
APPLICANT: Chemault, Ruth A.
APPLICANT: Meagher, Madelein Joy
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561PC
CURRENT FILLING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 2606
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Best Local Similarity
Matches 503; Conserv
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LOCATION: 411
OTHER INFORMATION: n =
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Pred. No. 2.3e-223;
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THERAPY

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RESULT 11
PCT-US01-43704-1161/c
Sequence 1161, Application PC/
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
APPLICANT: Stolk, John A.
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Best Local !
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Pred. No. 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 20121.561PC
CURRENT APPLICATION NUMBER: PCT/US01/43704
CURRENT FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 1161
LENGTH: 622
TYPE: DNA
CPCANTSM: HOMO Sapiéns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiéns
; FEATURE;
; NAME/KEY: misc_feature
; LOCATION: 615
; OTHER INFORMATION: n = A
PCT-USO1-43704-1161
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Score 509; DB Pred. No. 2.6e 0; Mismatches

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Application US/10146502

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Mismatches

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APPLICANT: Xu, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, ANI
ITILE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PRI
ITILE OF INVENTION: THERAPY OF BREAST CANCER
ITILE OF INVENTION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: US/20/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13409
LENGTH: 1150
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US-10-198-846-13409
Convence 13409, A
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Query Match
Best Local Similarity
                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: 1149, 1150
OTHER INFORMATION: n = 1
3-10-198-846-13409
                                                                                                                    ORGANISM: Homo sapiens
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 DB 6;
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Sequence 11863/c

Sequence 11863, Application US/09919002

GEMERAL INFORMATION:
APPLICANT: Leshkowitz, Dena
APPLICANT: Liu, Jin
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM:
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-752CON1
CURRENT APPLICATION NUMBER: US/09/919,002
CURRENT APPLICATION NUMBER: US/09/919,002
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09,
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: DATE: 1998-07-22
PRIOR APPLICATION NUMBER: FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 13203
SOFTWARE: FRASSEQ FOR WINDOWS Version 3.0
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                                                   SEQ ID NO 11863
LENGTH: 1309
ORGANISM: HOMO
-09-919-002-11863
                                      TYPE: DNA
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APPLICANT: OTSUKI, TETSUJI

TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEI

FILE REFERENCE: 084335/0123

CURRENT APPLICATION NUMBER: US/09/629,469A

CURRENT FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: JP 1999-248036

PRIOR FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: JP 1999-300253

PRIOR APPLICATION NUMBER: JP 2000-118776

PRIOR FILING DATE: 1999-08-27

PRIOR FILING DATE: 2000-01-11

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: JP 2000-183767

PRIOR APPLICATION NUMBER: JP 2000-183767

PRIOR APPLICATION NUMBER: JP 2000-241899

PRIOR APPLICATION NUMBER: JP 2000-241899

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: 60/159,590

PRIOR PRICING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: 60/183,322

PRIOR FILING DATE: 2000-02-17

NUMBER: OF SEO ID NOS: 19025
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11009
LENGTH: 1244
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LOCATION: (35)..(1102)
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ORGANISM: Homo sapiens
FEATURE:
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Pred. No. 0;
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Sequence 3468, Application US/09705256A
GENERAL INFORMATION:
APPLICANT: Ma, Xiao-Jun; Dotson, Stanton B.: Mons
TITLE OF INVENTION: Tumor Associated Molecules (TI
TITLE OF INVENTION: and prevention of cancer
FILE REFERENCE: 3214
CURRENT APPLICATION NUMBER: US/09/705,256A
CURRENT FILING DATE: 199-05-11
PRIOR APPLICATION NUMBER: US 60/164,285
PRIOR TILING DATE: 199-11-05
NUMBER OF SEQ ID NOS: 8259
SEQ ID NO 3468
LENGTH: 1234
TYPE: DNA
ORGANISM: Homo Sapiens
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99.7%;
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Pred. No. 0;
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Best Local Similarity
Matches 955; Conserva
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LOCATION: (1322)
OTHER INFORMATION: 0-10-219-793-106
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LOCATION: (1321)
OTHER INFORMATION:
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LENGTH: 1322
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DR FILLING DATE: 1997-07-08
DR FILLING DATE: 1997-07-08
DR FILLING DATE: 1997-08-18
DR APPLICATION NUMBER: 60/058,665
DR FILING DATE: 1997-09-12
DR APPLICATION NUMBER: 60/058,668
DR FILING DATE: 1997-09-12
DR APPLICATION NUMBER: 60/058,669
DR FILING DATE: 1997-09-12
DR APPLICATION NUMBER: 60/058,669
DR FILING DATE: 1997-09-12
OR APPLICATION NUMBER: 60/058,750
DR APPLICATION NUMBER: 60/058,751
OR APPLICATION NUMBER: 60/058,971
OR APPLICATION NUMBER: 60/058,971
OR APPLICATION NUMBER: 60/058,971
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RR FILING DATE: 1997-09-12
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RR FILING DATE: 1997-09-12
RR APPLICATION NUMBER: 60/06
RR FILING DATE: 1997-10-02
RR FILING DATE: 1997-10-02
RR FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60
FILING DATE: 1997-06-1
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FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/050,901
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APPLICATION NUMBER: 60
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FILING DATE: 1997-10-02
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OF SEQ ID NO
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APPLICANT:
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APPLICANT:

YAMAMOTO, JUNIO ISHII, SHIZUKO HAYASHI, KOJ SAITO, KAORU

JUNICHI

US-09-629-469A-11009; Sequence 11009, Application; GENERAL INFORMATION:

US/09629469A

APPLICANT: OTA, TOSHIO APPLICANT: ISOGAI, TAI

ISOGAI, TAKAO NISHIKAWA, TETSUO HAYASHI, KOJI

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                                   TCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCACC
                                                                                                                      CAACATAATGGAGATGCAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGTTC
                                                                                                                                                 gttctggcgaaggccaaggctaaagctgaagctattcgaatcctggctgcagctctgaca
                                                                                                                                                            GTTCTGGCGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACA
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        ACTCCAGACTCACTCTCCAGTGGGAGCAGCAGAGATGTCCAGGGTACAGATGCAAGT
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actccagactcactctccagtgggagcagcagaatgtccagggtacagatgcaagt
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APPLICANT: Webrmen, Tom
APPLICANT: Webrmen, Tom
APPLICANT: Ma, Yunging
APPLICANT: Zhao, Ping
APPLICANT: Zhao, Oing A.
APPLICANT: Zhao, Oing A.
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION NUMBER: US/10/119,428
CURRENT APPLICATION NUMBER: US/10/119,428
CURRENT APPLICATION NUMBER: 09/596,193
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/5719,705
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 55
SOFTWARR: Pt_Genes Version 1.0
SEQ ID NO 37
LENGTH: 9098
TYPE: DNA
OPCANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (75)..(9098)
US-10-119-428-37
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GENERAL INFORMATION:
APPLICANT: Tang, Y. T
APPLICANT: Liu, Chen
APPLICANT: Asundi, V
APPLICANT: Wa, Chong
APPLICANT: Wehrman,
APPLICANT: Ren, Feiy
APPLICANT: Wa, Yundi,
APPLICANT: Zhou, Pin
APPLICANT: Zhoo, Qin
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US-10-119-428-37
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Best Local Similarity
Matches 957; Conserv
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Asundi, Vinod
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Wehrman, Tom
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FILE REFERENCE: PZ008PIC1
CURRENT APPLICATION NUMBER: US/10/219,793
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/209,462
PRIOR FILING DATE: 1998-12-11
PRIOR PPLICATION NUMBER: PCT/US98/12125
PRIOR APPLICATION NUMBER: 60/049,547
PRIOR APPLICATION NUMBER: 60/049,547
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR FILING DATE: 1997-06-13
PRIOR PPLICATION NUMBER: 60/049,549
PRIOR PPLICATION NUMBER: 60/049,549
PRIOR APPLICATION NUMBER: 60/049,549
PRIOR APPLICATION NUMBER: 60/049,550
PRIOR APPLICATION NUMBER: 60/049,550
PRIOR APPLICATION NUMBER: 60/049,566
PRIOR APPLICATION NUMBER: 60/049,566
PRIOR APPLICATION NUMBER: 60/049,606
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,607
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,607
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,607
PRIOR FILING DATE: 1997-06-13
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RESULT 4
US-10-198-846-12975
Sequence 12975, Application US/10198846
Sequence 12975, Application US/10198846
GENERAL INFORMATION:
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Weng, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PRE
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 1909, 19
; OTHER INFORMATION: n = 1
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PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: PASTSEQ for Windows Version
SEQ ID NO 12975
LENGTH: 1910
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TYPE: DNA
ORGANISM: Homo
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PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/060,865
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,059
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
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FEATURE:
NAME/KEY: SITE
NAME/KEY: (1337)
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NAME/KEY: SITE
LOCATION: (1336)
OTHER INFORMATION:
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TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (1335)
OTHER INFORMATION: n
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                                                               TGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAG
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                                                                                                     actgctggggtatccgctgcctccgttatgagatcaaggatatccatgtgccaccccggg
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; NAME/KEY: misc_feature
; LCCATION: 1841, 1842
; COTHER INFORMATION: n = A,T,C
US-09-785-276A-24973
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PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
                                                                                                      Query Match
Best Local S
Matches 957
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SOFTWARE: FastSEQ for
SEQ ID NO 24973
LENGTH: 1842
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APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METI
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
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PRIOR FILING DATE: 2000-03-16
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PRIOR APPLICATION NUMBER: PCT,
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/0
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BR FILING DATE: 1997-06-13
BR APPLICATION NUMBER: 60/04
BR FILING DATE: 1997-06-13
                                                                                                                                                            FILING DATE: 1997-09-1
                                                               APPLICATION NUMBER: 60/0
FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/0
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APPLICATION NUMBER: 60
FILING DATE: 1997-09-1
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FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/0
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FILING DATE: 1997-10-02
APPLICATION NUMBER: 60/
FILING DATE: 1997-10-02
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FILING DATE: 1997-07-08
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          Match Length
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Gapop 60.0 , Gapext 60.0
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/cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
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          DB
     US-09-785-276A-24973
US-10-1194-28-37
US-10-1194-28-37
US-10-219-793-106
US-09-629-469A-11009
US-09-705-256A-3468
US-10-1198-846-13409
US-09-705-256A-3468
US-10-128-846-13409
US-09-919-002-11863
PCT-US01-43704-1841
PCT-US01-43704-58
US-10-214-403-2995
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US-10-214-403-2873
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US-09-918-995-333
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US-09-721-544-8507
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(without alignments)
11832.429 Million cell updat
Sequence 2, Appli Sequence 24973, A Appl Sequence 12975, A Sequence 106, Appl Sequence 11009, A Sequence 11408, A Appl Sequence 11463, A Sequence 11863, A Sequence 1161, Appl Sequence 1935, Appl Sequence 1075, Appl Sequence 1075, Appl Sequence 1075, Appl Sequence 1428, Appl Sequence 14
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US-10-198-846-5820	US-09-539-331D-30091	US-10-198-846-6734	US-09-785-276A-7770	US-09-539-331D-14079	US-09-540-210B-7087	US-09-540-210B-26126	US-09-539-331D-15486	US-09-539-331D-9558	US-09-539-331D-12906	US-09-539-331D-16278	US-10-097-105-596	US-09-629-469A-1950	US-09-540-210B-6996	US-09-540-210B-18465	US-09-539-331D-688	US-09-539-331D-21791	US-09-539-331D-15714	US-10-124-805-26	PCT-US02-12378-26
Sequence 5820, Ap	Sequence 30091, A	Sequence 6734, Ap	Sequence 7770, Ap	Sequence 14079, A	Sequence 7087, Ap	Sequence 26126, A	Sequence 15486, A	Sequence 9558, Ap	Sequence 12906, A	Sequence 16278, A	Sequence 596, App	Sequence 1950, Ap	Sequence 6996, Ap	Sequence 18465, A	Sequence 688, App	Sequence 21791, A	Sequence 15714, A	Sequence 26, Appl	Sequence 26, Appl

ALIGNMENTS

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; LIBRARY: Consensus
; CLONE: Consensus
; SEQUENCE DESCRIPTION: SEQ ID
US-09-898-216-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-898-216-2; Sequence 2, Application US/09898216; GENERAL INFORMATION:
                                                                                                                                                                                              TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,216
FILING DATE: 02-Jul-2001
CLASSIFICATION: Unknown>
                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/781,562
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-018
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOLI, Surya K.
TITLE OF INVENTION: NOVEL
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                                                                                                             LENGTH: 1188 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TYPE: DNA
CORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1296)...(264)
OTHER INFORMATION: Stanilar to 912984585 in th
OTHER INFORMATION: Run with FASTXX 3.3t00, de
US-09-496-914A-8410
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Best Local
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NUMBER OF SEQ ID NOS: 10410
SOFTWARE: pt_CT_genes Version 1.02
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OR APPLICATION NUMBER: US 60/125,453
OR FILING DATE: 1999-03-19
OR APPLICATION NUMBER: US 60/126,605
OR FILING DATE: 1999-03-26
OR APPLICATION NUMBER: US 09/306,350
OR FILING DATE: 1999-05-07
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RAPPLICATION NUMBER: US 05
REFILING DATE: 1999-02-12
DR APPLICATION NUMBER: US 05
DR FILING DATE: 1999-03-18
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APPLICATION NUMBER: NOT YET
FILING DATE: 1999-01-19
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APPLICATION NUMBER: US 09/399,720
FILING DATE: 1999-09-21
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FILING DATE: 1999-0
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                  CCTGGGTGGTGGAGCGAATGGGCCGATTCCACCGGATCCTGGAGCCTGGTTTGAACATCC 259
TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG
                                                                                                                                                                                         ACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCG
                                                                                                                                                                                                                                                   TGCCTGAGCAGTCGGCTGTGACTCTCGACAATGTAACTCTGCAAATCGATGGAGTCCTTT
                                                                                                                               TCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCAAACTCTCTNTGGACAAAG 499
                                                                                                                                                                           ACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCG
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                                                                                                                 TCACCCAGCTAGCTCAAACCAACCATGAGATCAGAGCTCGGCAAACTCTCTCGGACAAAG
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1999-04-15
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99.8%;
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Search completed: Job time: 6820 sec September 22, 2002, 18:14:09

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NAME/KEY: misc_feature

LOCATION: (1296)...(264)

OTHER INFORMATION: similar to gi2984585 in the genepept database release 114,

OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters

US-09-471-275-865
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EARLIER FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: US 09/274,861
EARLIER FILLNG DATE: 1999-03-23
EARLIER FILLNG DATE: 1999-03-23
EARLIER FILLNG DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-26
EARLIER FILING DATE: 1999-03-26
EARLIER FILLNG DATE: 1999-03-26
EARLIER FILLNG DATE: 1999-03-27
EARLIER APPLICATION NUMBER: US 09/306,350
EARLIER FILLNG DATE: 1999-05-07
EARLIER FILLNG DATE: 1999-09-21
EARLIER FILLNG DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 10451
SOFTWARE: pt_CCT_genes Version 1.0
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SEQ ID NO 865
*FNGTH: 1398
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Best Local S
Matches 957
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ER FILING DATE: 1999-01-22
ER APPLICATION NUMBER: US 09/240,371
ER FILING DATE: 1999-01-29
ER APPLICATION NUMBER: US 09/277,227
ER FILING DATE: 1999-03-25
ER APPLICATION NUMBER: US 09/271,490
ER FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                                                                                                                                    ACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCG 439
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US-09-496-914A-8410/c
Sequence 8410, Application US/09496914A
GENERAL INFORMATION:
APPLICANT: Tang, Yuanhua T.
APPLICANT: Tillinghast, John
APPLICANT: Tillinghast, John
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 787
CURRENT APPLICATION NUMBER: US/09/496,914A
CURRENT FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/333,690
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 09/034,341
PRIOR APPLICATION NUMBER: US 09/034,341
PRIOR APPLICATION NUMBER: US 09/0321,214
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR APPLICATION NUMBER: US 09/31,598
PRIOR APPLICATION NUMBER: US 09/31,597
PRIOR APPLICATION NUMBER: US 09/31,597
PRIOR APPLICATION NUMBER: US 09/31,517
PRIOR APPLICATION NUMBER: US 09/32,782
PRIOR APPLICATION NUMBER: US 09/32,510
PRIOR APPLICATION NUMBER: US 09/346,956
PRIOR APPLICATION NUMBER: US 09/346,956
PRIOR APPLICATION NUMBER: US 09/362,510

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CURRENT APPLICATION NUMBER: PCT/USO1/04098A
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: Not Yet Assigned
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 09/728, 422
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/63,561
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/63,325
PRIOR APPLICATION NUMBER: 09/63,936
PRIOR APPLICATION NUMBER: 09/62,325
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/520,325
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
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PCT-US01-04098A-2212/c
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; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-04098A-2212
                                                                                      Query Match
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Matches 957
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TITLE OF INVENTION: Novel
FILE REFERENCE: 21272-029
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GGACTCCAGACTCACTCTCCAGTGGGAGCAGCAGAGATGTCCAGGGTACAGATGCAAGT
                                             GCCGCGCCTCCTGGATTGCCCCGAAACACCGTGGTACTGTTCGTGCCGCAGCAGGAGG
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TCTCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCA 979
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RESULT 14
US-09-471-275-865/c
US-09-471-275-865/c
Sequence 865, Application US/09471275
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 782
CURRENT APPLICATION NUMBER: US/09/471,275
CURRENT FILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: US 09/235,076
EARLIER FILING DATE: 1999-01-20

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CURRENT FILING DATE: 2001-03-13;
PRIOR APPLICATION NUMBER: US 09/338,467;
PRIOR FILING DATE: 1999-06-22;
PRIOR FILING DATE: 1998-06-22;
NUMBER OF SEQ ID NOS: 1022;
SOFTMARE: FRASEQ for Windows Version 4.0;
SEQ ID NO 941;
LENGTH: 1384;
TYPE: DNA
ORGANISM: Homo sapiens
US-09-808-384-941
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                                                         CACAACATAATGGAGATGCAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGT
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cacaacataatggagatgcagcagcttcactgactgtggccgagcagtatgtcagcgcgt
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Pred. No. 0;
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APPLICANT: Tang, Y, Tom et al
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Pol
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: PCT/US01/03800A
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 09/580,875
PRIOR APPLICATION NUMBER: 09/580,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 1001
LENGTH: 1398
TYPE: DNA
ORGANISM: HOMO Sapiens
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                     TGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAG
                                                           ACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGG
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PRIOR APPLICATION NUMBER: 60/15
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9677
SOFTWARE: FASKSEQ for Windows V.
SEQ ID NO 7997
LENGTH: 1384
TYPE: DNA
ORGANISM: Homo sapiens
US-09-652-914-7997
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                                  Query Match
Best Local Similarity
Matches 957; Conserv
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CURRENT APPLICATION NUMBER: US/09/652,914
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,112
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TITLE OF INVENTION: NOVEL NU
TITLE OF INVENTION: THEREFOR
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GCCGCGCCTCTCTGGATTGCCCCGAAACACCGTGGTACTGTTCGTGCCGCAGCAGGAGG
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US-09-808-384-941

Sequence 941, Application GENERAL INFORMATION:

US/09808384

APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICAT: HOLTZMAN, DOUGLES A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED
TITLE OF INVENTION: HUMAN PROSTATE STROMAL LIBRARY
FILE REFERENCE: 1600.1025-002
CURRENT APPLICATION NUMBER: US/09/808,384

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ggactccagactcactctccagtgggagcagcagagatgtccagggtacagatgcaagt
                      GGACTCCAGACTCACTCTCCAGTGGGAGCAGCAGATGTCCAGGGTACAGATGCAAGT
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                                                       CCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTCACCAAAGCCCCAGTGCCAG 1039
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Sequence 7419, Application US/09652816
GENERAL INFORMATION:
APPLICANT: GULTIEREZ-Ramos, JOSE-CARIOS
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLE
TITLE OF INVENTION: THEREFOR
FILLE REFERENCE: 1600.1177-001
CURRENT APPLICATION NUMBER: US/09/652,816
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 06/152,111
PRIOR APPLICATION NUMBER: 06/152,111
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9647
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7419
LENGTH: 1384
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tgaaagagtctatgcagatgcaggtggaggcagagcggcggaaacgggccacagttctag
                                                   actgctggggtatccgctgcctccgttatgagatcaaggatatccatgtgccaccccggg
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Pred. No. 0;
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; LENGTH: 1384
; TYPE: DNA
; ORGANISM: HOMO :
US-09-652-913-8809
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOI
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1174-001
CURRENT APPLICATION NUMBER: US/09/652,913
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,107
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEO ID NOS: 10833
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8809
LENGTH: 1384
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GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/652,12

CURRENT FILING DATE: 2000-08-30

PRIOR APPLICATION NUMBER: 60/151,134

PRIOR FILING DATE: 1999-08-30

NUMBER OF SEO ID NOS: 10475

SOFTWARE: FastSEQ for Windows Version 4

SEO ID NO 7358

LENGTH: 1384
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Best Local Similarity
Matches 957; Conser
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                                            CACAACATAATGGAGATGCAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGT
                                                                                       actgctggggtatccgctgcctccgttatgagatcaaggatatccatgtgccaccccggg
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                              cacaacataatggagatgcagcagcttcactgactgtggccgagcagtatgtcagcgcgt
                                                                                                                       CAGTTCTGGCGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGA
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APPLICANT: Richardson, Jennifer
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES ANI
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600,1181-001
CURRENT APPLICATION NUMBER: US/09/649,162
CURRENT ETLING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,057
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9990
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US-09-649-162-7309
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; ORGANISM: Homo sapiens
US-09-649-162-7309
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SEQ ID NO 7309
LENGTH: 1384
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Best Local Sim:
Matches 957;
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                TGCCTGAGCAGTCGGCTGTGACTCTCGACAATGTAACTCTGCAAATCGATGGAGTCCTTT
                                                               TCATCCCTGTGTTAGACCGGATCCGATATGTGCAGAGGTCTCAAGGAAATTGTCATCAACG
                                                                                                                              CCTGGGTGGTGGAGCGAATGGGCCGATTCCACCGGATCCTGGAGCCTGGTTTGAACATCC
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                                               tcatccctgtgttagaccggatccgatatgtgcagagtctcaaggaaattgtcatcaacg
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Pred. No. 0;
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.1180-001
CURRENT APPLICATION NUMBER: US/09/652,109
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,128
PRIOR APPLICATION NUMBER: 60/151,128
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 10105
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7925
; ORGANISM: Homo US-09-652-109-7925
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GENERAL INFORMATION:
APPLICANT: MCCarthy, Sean A.
                                  TYPE: DNA
                                                   LENGTH:
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; SEQ ID NO 941
; LENGTH: 1384
; TYPE: DNA
; ORCANISM: Homo sapiens
US-09-338-467-941
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Best Local Similarity
Matches 957; Conser
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CURRENT FILING DATE: 1999-06-22
EARLIER APPLICATION NUMBER: 60/090,177
EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 1022
SOFTWARE: FastSEQ for Windows Version 3.0
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                                      cacaacataatggagatgcagcttcactgactgtggccgagcagtatgtcagcgcgt
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US-09-644-869-8024
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APPLICANT: McCarthy, Sean A.
APPLICANT: McCarthy, Sean A.
APPLICANT: Moltaman, Douglas A.
APPLICANT: Monahan, John
APPLICANT: Richardson, Jennifer
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLE
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1182-001
CURRENT APPLICATION NUMBER: US/09/644,869
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,062
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9708
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SEQ ID NO 8024
FENGTH: 1384
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Best Local S
Matches 957
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TYPE: DN
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ORGANISM: Homo
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FastSEQ for Windows Version
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SOFTWARE: PatentI
SEQ ID NO 45
LENGTH: 1337
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LOCATION: (1336)
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NAME/KEY: SITE
LOCATION: (1337)
OTHER INFORMATION: r
S-09-209-462B-45
                                                                                                                                      NAME/NE (1337)
LOCATION: (1337)
OTHER INFORMATION: r
NAME/KEY: SITE
NAME/KEY: (1336)
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       Query Match
Best Local Similarity
Matches 957; Conser
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RAPPLICATION NUMBER: 60/051,919

DR FILING DATE: 1997-07-08

DR APPLICATION NUMBER: 60/055,984

DR FILING DATE: 1997-08-18

DR FILING DATE: 1997-08-18

OR FILING DATE: 1997-09-12

OR APPLICATION NUMBER: 60/058,668

OR FILING DATE: 1997-09-12

OR FILING DATE: 1997-09-12
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DR APPLICATION NUMBER: 60/04
DR APPLICATION NUMBER: 60/06-13
DR APPLICATION NUMBER: 60/06-13
DR FILING DATE: 1997-06-13
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DR APPLICATION NUMBER: 60/04
DR FILING DATE: 1997-06-13
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APPLICATION NUMBER: 60/C
APPLICATION NUMBER: 60/C
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FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/058,975
APPLICATION NUMBER: 60/058,975
APPLICATION NUMBER: 60/058,975
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FILING DATE: 1997-10-02
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FILING DATE: 1997-10-02
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          Conservative
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1997-09-12
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                    Score 857;
Pred. No.
        Mismatches
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                                  16;
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                                  Length 1337;
       0,
     Gaps
       0;
US-09-338-467-941

; Sequence 941, Application US/09338467
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PZ00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8439
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
PCT-US98-12125-45
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MEDIUM TYPE: DISKette, 3
COMPUTER: HP Vectra 486,
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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FILING DATE: Jan 01, 1
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Scient STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
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5 US-60-172-373-10483
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8 US-9-878-134-349
7 US-10-033-356-349
7 US-09-359-922-11863
7 US-09-98-598-1161
3 US-09-98-598-1161
3 US-09-98-598-1193
7 US-10-046-935-193
7 US-10-081-124-244
7 US-10-081-124-2495
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7 US-09-652-127-341
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US-09-209-462B-45
(Sequence 45, Application US/09209462B
(GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 86 Human Secreted Proteins
FILE REFERENCE: P2008P1
CURRENT APPLICATION NUMBER: US/09/209,462B
CURRENT FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: PCT/US98/12125
PRIOR APPLICATION NUMBER: 60/049,547
PRIOR APPLICATION NUMBER: 60/049,547
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
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PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR APPLICATION NUMBER: 60/049,548

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Post-processing: Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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/Cgn2_6/ptodata/1/pna/US07_COMB.seq:*
/Cgn2_6/ptodata/1/pna/US080_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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US-09-340-623-13379 US-09-898-888-13379 US-09-898-888A-13379 PCT-US01-04098A-244 US-09-598-075-249	US-09-652-914-7997 US-09-652-914-7997 US-09-652-914-7997 US-09-684-941 PCT-US01-03800A-1001 PCT-US01-03800A-1212 US-09-471-275-865 US-09-496-914A-8410 US-09-560-875A-8410 US-09-298-733-35 US-09-298-733-35 US-09-298-733-35 US-09-724-497-35 US-09-724-497-35 US-09-724-497-37 PCT-US01-08656-5097 PCT-US01-08656-5097 PCT-US01-08656-5097 US-09-205-070-13379	- 600 - 600	ID
Sequence 13379, A Sequence 13379, A Sequence 13379, A Sequence 244, App Sequence 249, App	sequence 809, Ap Sequence 7997, Ap Sequence 7997, Ap Sequence 1001, Ap Sequence 1001, Ap Sequence 2212, Ap Sequence 865, App Sequence 8410, Ap Sequence 8410, Ap Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 37, Appl Sequence 106, App Sequence 106, App Sequence 106, App	45, Apr 45, Apr 941, 1 8024, 7309, 7925, 7358,	Description

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Search completed: September 22, 2002, 17:24:48 Job time: 7095 sec	Matches 17; Conservative 0; Mismatches Oy 554 CTGCTGACTGCTGGGGT 570	Best Local Similarity 100.0%; Pred. No. 44;
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         CACCAAAGCCCCAGTGCCAGGGACTCCAGACTCTCTCCAGTGGGAGCAGCAGCAGAGATGT
                                                                                                                    AGGGAAGAAACAGGCCCAGATCCTGGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCA
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-femail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
DNA Sequencing by: National Institutes of Health Int
Sequencing Center (NISC),
Gaithersburg, Maryland;
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 5 Row: m Column: 8
This clone was selected for for form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brook
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legasy
Lim,M., Maduro,O.L., Masiello,C., Mastrian,S.D., McCloskey,J.C
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,P.
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (05-FEB-2001) National Institutes of He Gene Collection (MGC), Cancer Genomics Office, Na Institute, 31 Center Drive, Room 11A03, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens, complete cds.
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BC002442.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone was selected for full length sed the following selection criteria:
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/protein_id="AAH02442.1"
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/db_xref="Gi:12803255"
/translation="MLARAARGTGALLLRGSLLASGRAPRRASSGLPRNTVVLFVPQQ
EAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEOSAVTLDNVTLQID
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EAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEOSAVTLDNASIVDA
IVVALRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSLDKVVRERESSLNASIVDA
INQAADCWGIRGLRYEIKDIHVPPRVKESMQMOVEAERKRATVLESEGTRESAINVA
EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASL
TVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSG
                                                                                                                                                                                                                        /note="Vector: pOTB7"
47. .1117
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/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="LocusID:30968"
/db_xref="taxon:9606"
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Catarrhini; Hominidae
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MGC:1179 IMAGE:3346384, mRNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing because
: matched mRNA gi:
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National Cancer
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Cytogenet.
21328876
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A novel member of the STOMATIN/EPB72/mec-2 family,
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AF282596
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Mammalia; Eutheria;
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EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASL
TVAEQYVSAFSKLAKSSNTILLESNPGDVTSHVAQAMGVYGALTKAPVPGTPDSLSSG
SSRDVQGTDASALDEELDRVKMS"
1222. 1227.
                                                                       /protein_id="AAF91466.1"
/protein_id="AAF91466.1"
/db_xref="01:9652259"
/translation="MLARAARGTGALLLRGSLLASGRAPRRASSGLPRNTVVLFVPQQ
/translation="MLARAARGTGALLLRGSLLASGRAPRRASSGLPRNTVVLFVPQQ
/translation="MLARAARGTGALLLRGSLLASGRAPRRASSGLPRNTVLDNTTLQID
CAWVVERMGREHRILEPGLNILIPVLDRIRYVQSLKEIVINVERGEQSAVTLDNTTLQID
GVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSLDKVFRERESLNASIVDA
INQAADCWGIRCLRYEIKDIHVPPRVKESMOMQVEAERRKRATVLESEGTRESAINVA
                                                                                                                                                                                                                                                 /note="member of the stomatin/band7/EPB72/MEC2 family: similar to the predicted Caenorhabditis elegans protei F30A10.5, to Caenorhabditis elegans MEC-2, and to the
                                                                                                                                                                                                                                                                                                                              /gene="SLP2"
3,5...1105
                                                                                                                                                                                                                               sapiens stomatin
                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                       /product="stomatin-like protein
/protein_id="AAF91466.1"
                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="brain"
/dev_stage="fetus"
1. .1260
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                                 TGGCCAAGGACTCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCACCAGCATGG 988
                                                                                 ATGGAGATGCAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGTTCTCCCAAAC 928
                                                                                                                                   CGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTTGACACACATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jb, Tel:81-438-52-3951), Fax:81-438-52-3952)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-6 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
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Homo sapiens teratocarcinoma cell_line:NT2 cDNA
clone_lib:NT2RM1 clone:NT2RM1000080.
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Isogai, T. and Otsuki, T.
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                /protein_id="BAB55091.1"
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/tanslation="MLARARGTGALLLRGSLLASGRAPRRASSGLPRNTVVLEVPQQ
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EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKARAERILAAALTQHNGDAAASL
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TVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSG
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                                                                                                                                                                                                                                                                                                                           /cell_type="teratocarcinoma"
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TGGCCAAGGACTCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCACCAGCATGG 988
                                    ATGGAGATGCAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGTTCTCCAAAC
                                                                         CCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGAGGCCAGTGCAGTTCTGG
                                                                                                                                                  GGACCCGAGAGTCGGCCATCAATGTGGCAGAAGGGAAGAAAACAGGCCCAGATCCTGGCCT
                                                                                                                                                           GGACCCGAGAGTCGGCCATCAATGTGGCAGAAGGGGAAGAACAGGCCCAGATCCTGGCCT
                                                                                                                                                                                      CTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAGAGTCTGAGG
                                                                                                                                                                                                 CTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAGAGTCTGAGG
                                                                                                                                                                                                                                                                                                                                      TCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCGTCACCCAGC
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                                                                                          CGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACACAACATA 868
                                                                                                              CCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCCAGTGCAGTTCTGG
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BC010152
                                                                                                                                                                                                                                                                                                                                Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be fo through the I.M.A.G.E. Consortium/LLNL at: http://image.linl.gov Series: IRAL Plate: 27 Row: d Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUL-2001) National Institutes of Headene Collection (MGC), Cancer Genomics Office, Nat Institute, 31 Center Drive, Room 11A03, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC010152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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mmalia; Eutheria; Primates; Catarrhini; Hominidae;
(bases 1 to 1281)
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lete cds.
                                                                                                                                                                                                   to protein.
                                                                           /organism-"Homo sapiens"
/db_xref="Locusid:30968"
/db_xref="Laxon:9606"
/clone="MGC:19715 IMAGE:3534656"
                                                                                                                                                                               Location/Qualifiers
/note="Vector:
                /lab_host="DH10B-R"
                                   /tissue_type="Lung, small
/clone_lib="NIH_MGC_7"
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da, MD 20892-2590,
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IMAGE:3534656, mRNA,
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                                                                                                 GGACCCGAGAGTCGGCCATCAATGTGGCAGAAGGGAAGAAACAGGCCCAGATCCTGGCCT 748
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53; Conservative
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/product="stomatin-like 2"
/product="aAH10152.1"
/db_xref="GI:1460403"
/translation="mlaraargTgalllrgSllasgraprrassglprnvtvvlfvpQQ
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GVLYLRIMDPYKASYGVEDPEYAVTOPAOTTMRSELGKLSJDKVFRERESLNASIVDA
INQAADCWGIRCLBYEIKDIHVPPRVKESMQMQVEAERKRATVLESEGTRESAINVA
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INQAADCWGIRCLBYEIKDIHVPRVKESMQMQVEAERKRATVLEAALTQHNGDAAASL
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SSRDVQGTDASLDEELDBVKMS"
330 c 372 g 264 t
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Pred. No. 2.9e-258;
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CGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACACAACATA

848

FEATURES

clone was selected for fund the following selection

ll length sequencing
criteria: Similarity

to protein

/organism="Homo sapiens" /db_xref="LocusID:30968" Location/Qualifiers δõ

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COMMENT
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AUTHORS
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Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/ILML at: Series: IRAL Plate: 34 Row: p Column: 12 This clone was selected for full length sec
                                                                                        Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erlin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                       cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD:20892-2590,
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/tissue_type-"Pancreas, epithelioid
/clone_lib-"NIH_MGC_42"
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                                                                                                                                    DNA Sequencing by
BC Cancer Agency,
info@bcgsc.bc.ca
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
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Submitted (06-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/protein_id="AAH03025.1"
/db_xref="GI:12804333"
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/tissue_type="Lung, small cell
/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="LocusID:30968"
/db_xref="taxon:9606"
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                                                                                                                Submitted (21-NOV-2000) Department of Medical College Hospital, 2, Yuh-Der Location/Qualifiers
                                                                                                                                                                           Mammalla; Eutheria; Rodentia
1 (bases 1 to 1253)
Chang, J.G. and Chan, W.L.
Mouse stomatin-like protein
Unpublished
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Mus musculus stomatin-like
AF323178
AF323178.1 GI:12382776
                                                                                                                                                        2 (bases 1 to 1253)
Chang, J.G. and Chan, W.L.
                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                       house mouse
/codon_start=1
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/db_xref="GI:12382777"
                                                    /tissue_type="kidney"
32. .1093
                                                                                 /organism="Mus
/strain="FVB"
                                                                         /db_xref="taxon:10090"
                                          /note="MSLP2"
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AGATGCAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGCTTCTCCAAACTGGC
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EAMVVERWGRFHRILEPGLNVLLFVLDRIRYVQSLKEIV INVPEQQSAVTLDNVTLQID
GVLVLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSLDKVFREBESLJNANIVDA
INQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVA
EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAGALTQHNGDAAASL
TVAEQYVSAFSKLAKDSNTVLLPSNPSDVTSMVAQAMGVYGALTKAPVPGAQNSSQSR
RDVQATDTSIEELGRVKLS"
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Pred. No. 9.7e-196;
0; Mismatches 125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAACTCCAGCCAGAGCAGAAGAGATGTCCAGGCTACAGACACGAGTAT---TGAAGAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGGATTCCAACACAGTGCTACTGCCCTCCAATCCCAGCGACGTCACGAGTATGGTGGC
                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be fo
through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov
Series: IRAK Plate: 5 Row; k Column: 5.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale,
A.M., Holloway, M., Telford, B, H
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC003425 n 1565 bp n Mus musculus, RIKEN cDNA 0610038F01 IMAGE:2609584, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                             /note="Vector: 12. .1073
                                                                                                                                                    /clone="MGC:6777 IMAGE:2609584"
/tissue_type="Mammary tumor. C3(1)-Tag model.
ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
                /codon_start=1
/product="RIKEN CDNA 0610038F01
/protein_id="AAH03425.1"
/db_xref="GI:13097354"
translation="MLARAARGTGALLLRGSVQASGRVPRRASSGLPRNTVILFVPQQ/
                                                                                                                                      /lab_host="DH10B"
                                                                                                                                                                                                                                    /db_xref="LocusID:66592"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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Rodentia;
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Bouck,
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GCTATTCGAATCCTGGCTGCAGCTCTGACACACATAATGGAGATGCAGCAGCTTCACTG
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                                                         GCGATTCGAATTCTGGCTGGGGCTCTGACTCAACATAATGGAGATGCAGCAGCTTCGCTC
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35; Conservative
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GVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSLDKVERERESLNANIVDA
INQAADCWGIRCLRYBLKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVA
EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAEAIRILAGALTQHNGDAAASL
TVAEQYVSAFSKLAKDSNTVLLPSNPSDVTSMVAQAMGVYGALTKAPVPGAQNSSQSR
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87.98;
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Pred. No. 5.5e~192;
0; Mismatches 123;
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          ACTGCTGGGGTATCCGCTGCCTNCGTTATGAGÀTCAA-GGATATCCATGTGCCACCCCGG
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616; Conser
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AX261777
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Mammalia; Eutheria;
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/db_xref="taxon:9606"
168 c 184 g 140
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Primates;
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Pred. No. 2.5e
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128 04-OCT-2001;
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                                                                                             TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG
                   ACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCG 439
                                                                                                                                                                                                                                                                                               Homo Sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 518)
Xu,J., Lodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J.,
Stolk,J.A., King,G.E., Wang,T. and Jiang,Y.
Compounds for immunotherapy and diagnosis of colon cancer and
methods for their use
Patent: WO 0149716-A 1031 12-JUL-2001;
CORIXA CORPORATION (US)
CORIXA CORPORATION (US)
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Sequence 1031 from Patent W00149716
AX193464
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/db_xref="taxon:9606"
136 c 149 g 10
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Pred. No. 6.1e-112;
O; Mismatches 3;
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Best Local Similarity
Matches 455; Conserv
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                                                       CAAGGACTCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCACCAGCATGGTGGC
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TCAGGCCATGGGTGTATATGGAGCCCTCACCAAAGCCCCAGTGCCAGGGACTCCAGACTC 1052
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                                            CAAGGACTCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCACCAGCATGGTGGC
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patent: WO 0196388-A 193
CORIXA CORPORATION (US)
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Sequence 193 from Patent
AX339946
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Mammalia; Eutheria;
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/db_xref="taxon:9606"
123 c 137 g 7
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (16-SEP-2001) Human Genome Sequencing Center, Depai of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15625866.
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            Consensus quality: 152607, bases at least Q40 Consensus quality: 159995 bases at least Q30 Consensus quality: 167102 bases at least Q20 Estimated insert size: 161475; sum-of-contigs estimation quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                 Center project name: GEHL
Center clone name: CH230-14D17
------Summary Statistics
Assembly program: Phrap; version 0.990329First call
                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
Project Information
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft" sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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03-AUG-1998 (first entry) AAV28867 standard; DNA; 1188 BP

Human integral membrane protein encoding DNA.

Human; integral membrane protein; IMP; cancer; anaemia; prostate; breast; pancreatic; tumour; ion transport; ss.

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CC haematopoiesis regulatory activity; tissue growth activity:

CC immunomodulatory activity; activity: or inhibin-related activities:

CC chemotactic or chemokinetic activities; haemostatie thrombotic or

CC thrombolytic activities; receptor or ligand activities; or may be

CC involved in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of

CC invention are useful for preventing, treating or ameliorating medical

CC conditions, e.g., by protein or gene therapy. Such conditions include

CC conditions, e.g., by protein or gene therapy. Such conditions include

CC disorders, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC disorders, chronic inflammatory conditions (e.g., asthma or arthritis),

CC proliferative retinopathy, atherosclerosis, coronal heart disease,

CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

CC vascular growth. Polypeptides involved with tissue regeneration and

CC repair (or nucleic acids encoding them) may be used to promote wound

CC immunomodulatory activities may be used in the treatment of viral,

CC polypeptides with growth factor activity may be used in cell cultures to

CC polypeptides with growth factor activity may be used in cell cultures to

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC that can be used to augment or replace cells damaged by illness,

CC autolmune disease or accidental damage. The polypeptides and nucleotides

and in drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant bost cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of identifying compounds which bind to polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel many of the polypeptides of the invention have homology to known proteins, thereby glving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; as them cell growth factors activity; however, activity; activity; activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human proteins and DNA encoding sequences useful treating or ameliorating a medical condition in e.g. arthritis and cancer -
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27-APR-2000;
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19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment of cancer, leukaemia, nervous system disorders, inflammation.
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CAAACTCTCTNTGGACAAAGTCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGA
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13-JUN-1997;
13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
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                                                    CC Secreted human protein. The gene number, and the clone it is derived CC from, are detailed in the descriptor line. The gene can be used to CC generate fusion proteins by linking to the gene can human immunoglobulin CC Fc portion (e.g. AAX04302) for increasing the stability of the fused CC protein as compared to the human protein only.

CC acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225) CC which are useful for preventing, treating or ameliorating medical CC conditions e.g. by protein or gene therapy. Also, pathological CC conditions can be diagnosed by determining the amount of the new CC polypucleotides. Specific uses are described for each of the 86 CC polynucleotides, based on which tissues they are most highly expressed in CC (see AAX04311 for described uses).
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02-OCT-1997;
02-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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TGCCGTCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCAAACTCTCTNTGGA 494
                                           cctttacctgcgcatcatggacccttacaaggcaagctacggtgtggaggaccctgagta
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of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end cc sequence and an oligonucleotide comprising a sequence complementary to a complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to a cc oligonucleotide which comprises at least 15 nucleotides and the combination of ct the 5'-end sequence/3'-end sequence is selected from those defined in ct the specification. The primer sets can be used in antisense therapy and cc in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the cc detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB95893 represent human cand sequences; and AAH13629 to AAH13632 crepresent oligonucleotides, all of which are used in the exemplification of the present invention.
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                            full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly tfull-length cDNAs defined in the specification, and for the and/or diagnosis of the abnormality of the proteins encoded full-length cDNAs -
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Sugiyama
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2000JP-0183767.
2000JP-0241899.
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T, Wakamatsu
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C, Otsuki
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nilarity 99.4%;
Conservative
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Pred. No. 6e-3
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Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoissis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease
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07-MAR-2000;
19-MAY-2000;
17-JUN-2000;
14-JUL-2000;
                                                                                                                                                                                                                                                                                           multiple sclerosis; rheumatoid arthritis fertility; analgesic; pain; antigen; ss.
                                                                                                                                                                                                                                                                                                         gut protection; lung; liver fibrosis; immune deficiency; infection;
severe combined immunodeficiency; SCID; autoimmune disorder; allergy
multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
                   Tang
                                                                            19-SEP-2000;
20-OCT-2000;
                                                                                                                                                                              05-MAR-2001;
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                                               (HYSE-) HYSEQ
    QA,
                   Liu
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2000US-0574454.
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    C, Wehrman T, Zhang J, Chen
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WPI; prepared 2001-589934/66. polypeptides and nucleic acids obtained from cDNA libraries red from various human tissues, for diagnosis and treatment or, neurological, inflammatory, and autoimmune disorders of

Zhao

Yang

RT,

72

Claim ID No 107pp; English.

The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating confilmantory conditions such as arthritis, nephritis, Crohn's disease, cischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth can defend remodeling. (I), (II) and modulators of (II) are useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve cancers. (II) induces the proliferation of neural cells and regeneration of nerve cathery of the polypeptides. (II) is also useful for creating transgenic and is useful for the treatment of central and cell responses. Huntington's disease, and amyotrophic lateral continuity, regulation of haematopoiesis and neuropathies, such as Alzheimer's, cativity, regulation of haematopoiesis and is useful for treating myeloid cor lymphoid cell disorders, platelet disorders such as thrombocytopenia cultisue growth, and in tissue repair, healing of burns, incisions, culters, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, creperfusion injury in various tissues, various immune deficiencies and conditions, autoimmune disorders e.g. multiple sclerosis. Creactions and conditions, such as asthma or other respiratory problems. Cf. in addition, (I) affects blorhythms or circadian cycles of rhythms, cfatabolism, catabolism, anabolism, storage or elimination of distance of distance in the conditions of circadian cycles of rhythms. dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analyesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAS44920-AAS45295 represent novel human secreted proteicoding sequences of the invention. response. protein

Sequence 9098 B₽; 1918 A; 2538 C; 2590 ი : 2052 ₽; 0

Query Match Best Local Similarity 93 .3%; Score Pred. 1104 ŏ. 14.8; DB 2 2.8e-303; . 8; 22;

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RESULT
AAS58752
ID AAS5
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 Query Match
Best Local Similarity
Matches 616; Conser
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04-MAY-2000;
05-MAY-2000;
                                                                            Th present invention relates to the isolation of novel cDNA sequences encoding for at least an immunogenic portion of human colon tumour proteins. The sequences of the invention are useful in pharmaceutical compositions and vaccines for the prevention and treatment of cancers such as colon cancer. They are also useful for the diagnosis and monitoring of such cancers. Antibodies to the colon tumour proteins and antigen presenting cells that express polynucleotides encoding colon tumour proteins can be used to inhibit the development of cancers. T-cells that react specifically with colon tumour proteins are useful for removing tumour cells from samples (e.g. blood) and for cancer treatment. The polynucleotides sequences are also useful ir gene therapy. AAS57325-AAS58880 represent the cDNA sequences of the invention that encode for portions of human colon tumour proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                       treatment,
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2000US-202024P.
2000US-202189P.
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Score 516.6; DB 23;
Pred. No. 1.2e-136;
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RESULT 1
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AC AAK9
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OS Homc
XX Homc
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XX 08-0
PR 111-0
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11-JAN-2000;
02-MAY-2000;
    Example
                                              use in
                                                                                                           WPI; 2001-524255/58
                                                                                                                                                   Wakamatsu
                                                                                                                                                                         Ota T,
                                                                                                                                                                                                               (HELI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA clone representative sequence, SEQ ID NO: 1652.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  full length cDNA; cDNA synthesis; oligo-capping; ss
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; 2000JP-0118774.
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1652; 1380pp + sequence listing;
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T, Nagai
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K, Kojima
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T, Koga
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XEXEX

AAH05115 standard; cDNA;

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Human cDNA clone (5'-primer) 26-JUN-2001 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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                                                                           ggtatccgctgcctccgttatnanatc
                                                                                                              GGTATCCGCTGCCTNCGTTATGAGATC
                                                                                                                                        aacgggagtccctgaatgccagcattgtngatgccatccaaccaagctgctgantgctgg
                                                                                                                                                           AACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCAT-CAACCAAGCTGCTGACTGCTGG
                                                                                                                                                                                                                        TAGCTCAAACCATGAGATCAGAGCTCGGCAAACTCTCTNTGGACAAAGTCTTCCGGG
                                                                                                                                                                                                                                                                                      TCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCGTCACCCAGC
                                                                                                                                                                                                                                                                                                                                     agtcggctgtgactctcgacaatgtaactctgcnaatcgatggagtcctttacctgcgca
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97.0%;
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Pred. No. 1.3e-136;
D; Mismatches 14;
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CC full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary countries to the complementary strand of a polynucleotide which comprises one of countries of the 5002 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 5'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence, where the condition of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; and AAH13629 to AAH13620 cof the present oligonucleotides, all of which are used in the exemplification of the present invention.
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27-AUG-1999;
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      TGGAGCGAATGGGCCGATTCCACCGGATCCTGGAGCCTGGTTTGAACATCCTCATCCCTG
                                                               CCTCTGGATTGCCCCGAAACACCGTGGTGCTGTTCGTGCCGCAGCAGGAGGCCTGGGTGG
                                                                                                                                                CTGGGGCCCTTTTGCTGAGGGGCTCTCTACTGGCTTCTGGCCGCGCTCCG-GCCGCGCCT 148
                                                                                                                                                                                                                              ctggggcccttttgctgagggctctctactggcttctggccgcgctccgcgcgccct
                                          cctctggattgccccgaaacaccgtggtactgttcgtgccgcagcaggaggcctgggtgg
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Sugiyama
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; 2000JP-0183767.
; 2000JP-0241899.
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T, Wakama
                                                                                                                                                                                                                                                                                                               43.5%;
97.0%;
                                                                                                                                                                                                                                                                                                                                                                                             A; 162
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Pred. No. 1.3e-136;
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The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases
                                                                                                       Claim
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10-JAN-2000;
15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
29-JUN-2000;
28-AUG-2000;
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                           Colon tumor prevention,
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Page 415; 472pp;
                           associated diagnosis a
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CC expression, such as colonic cancer. For example, (I) and (II) may be
CC used to treat disorders associated with decreased expression by
CC rectifying mutations or deletions in a patient's genome that affect the
CC activity of TCAPs by expressing inactive proteins or to supplement the
CC patients own production of them. Additionally, (II) may be used to
CC produce the TCAP proteins, by inserting the nucleic acids into a host
CC complementary sequences may also be used as DNA probes in diagnostic
CC complementary sequences may also be used as DNA probes in diagnostic
CC quantitate the presence of similar nucleic acids in samples, and
CC quantitate the presence of similar nucleic acids in samples, and
CC also be used as antigens in the production of antibodies against TCAPs
CC and in assays to identify modulators of TCAP expression and activity.
CC and in assays to identify modulators of TCAP expression and activity.
CC TCAP expression and activity. The anti-(I) antibodies may also be used
CC as diagnostic agents for detecting the presence of TCAPs in samples
CC (e.g. by enzyme linked immunosorbant assay (ELISA)). AA128460 to AA129512
CC and AAM24494 to AAM24523 represent nucleotide and amino acid sequences
CC given in the exemplification of the present invention.
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14 - MAR - 2000;
24 - MAR - 2000;
29 - MAR - 2000;
15 - MAY - 2000;
09 - JUN - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides activity.
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TAGAGTCTGAGGGGACCCGAGAGTCGGCCATCAATGTGGCAGAAGGGAAGAAACAGGCCC
                                     GGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAG-AGCGGCGGAAACGGGCCACAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0189167.
2000US-0192099.
2000US-0193480.
2000US-0205230.
2000US-0211315.
2000US-0220534.
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            are also useful for isolating
                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001WO-US00798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3695pp;
                                                                                                                                                                                                                                                                                                                                                               40.3%;
88.7%;
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Mismatches
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11-JAN-2000;
02-MAY-2000;
                                                          clones. 830 cDNA molecules encoding a human protein have been solated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA clone representative sequence,
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AAK93925 standard; cDNA; 566 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUL-2000; 2000EP-0114089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1130094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; full length cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HELI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to primers for synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 11; SEQ ID NO 2385; 1380pp + sequence listing; English
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tsu A, Sugiyama T, Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genetic manipulation
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2000JP-0118774.
2000JP-0183765.
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K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full length cDNA clones and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO: 2385.
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S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ξ
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Query Match

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Score 465.6;

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Length 566

Sequence

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BP;

120 A;

152 C; 139

G; 155 T; 0 other;

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RESULT 15
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                                                                                                                           23-MAR-2000;
11-JUL-2000;
                                                                                                                                                      23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                           pharmaceutical; gene;
                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling;
                                                                                                                                                                                                                                                                         26-MAR-2002
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                       genes from Drosophila interactions
                                   New isolated nucleic acid genes from Drosophila and
                                                             WPI; 2001-656860/75.
P-PSDB; ABB61346.
                                                                                         Venter
                                                                                                                                                                       27-SEP-2001
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                                                                                         JC,
                                                                                         Adams M,
                                                                                                                            2000US-191637P
2000US-0614150
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Matches 578; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1153 BP; 298 A; 297 C;
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TCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCACCAGCATGGTGGCTCAGGCC
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                                                                                                       GCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGTTCTCCAAACTGGCCAAGGAC
                                                                                                                                                                                                         GCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACACAACATAATGGAGATGCA 879
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Db 916 aataacaccatgatcttgccctcgaatcccggggatgttaatggcttcgtggcccaggcc 975
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Db 976 ctggcggtgtacaaccacgtttccaa 1001

Search completed: September 22, 2002, 15:26:24 Job time: 4289 sec

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             Query Match
Best Local Similarity
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Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 15, Appl	Sequence 15, Appl	Sequence 15, Appl	Sequence 2, Appli	Sequence 2, Appl1	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 19, Appl	Sequence 5, Appli	Sequence 30, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

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US-08-781-562-2
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APPLICANT: Hillman, Jennifer L.
APPLICANT: GO11, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1188 base pairs
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                               FILING DATE: Herewith CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                      TELEPHONE: 415-855-0555
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                                                                                                  TYPE: nucleic acid
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    ACCAAAGCCCCAGTGCCAGGGACTCCAGACTCACTCTCCAGTGGGAGCAGCAGCAGAGATGTC
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
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US-08-232-463-14/c
; Sequence 14, Application
; Patent No. 5670367
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Best Local S
Matches 8
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CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 2313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VE
CURRENT APPLICATION DATA:
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT
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AGATCCTGGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCCCA
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8; Conserv
                                                                                                                                                                                                                                                                                                                          7218 base pairs
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                                                                                                                                                      Conservative
                                                                                                                                                    4.1%; Score 48.8; DB 1; 2.6%; Pred. No. 0.00051; vative 184; Mismatches 116;
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Best Local Similarity
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                                                                                                                                                                             Matches 153;
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APPLICANT: Duvic, Madeleine
APPLICANT: Schroeder, Wanda T
                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2488 base pairs
TYPE: nucleic acid
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TELEPHONE: 512/320-7200
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
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TELEPHONE: 512/474-7577
TO NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mayfield, Denise L. REGISTRATION NUMBER: 33,7 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: ConcurCLASSIFICATION: 43
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GGATGCCATCAACCAAGCTGCTGACTGCTGGGGGTATCCGCTGCCTNCGTTATGAGATCAA 596
                                                                                                                                          TGTGGAGGACCCTGAGTATGCCGTCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCT 476
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                                              CGGGACCCTGACAGTGGAGCAGATTTATCAGGACCGGGACCAGTTTGCCAAGCTGGTGCG
                                                                           CGGCAAACTCTCTNTGGACAAAGTCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGT 536
                                                                                                            TGTGCAGGACATCAAAAACGTCGTCCTGCAGACCCTGGAGGGACATCTGCGCTCCATCCT 323
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                                                                                                                                                                                          Score 39.6; DB Pred. No. 0.12;
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US-08-464-954A-1
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US-08-464-954A-1
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                                                                                                                            Matches
                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0
FILING DATE: June 11, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WORDPERFECT CURRENT APPLICATION DATA:
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                                                     1317 CCGACTACTGGGGCCTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCC 1376
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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617 GGGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAG 673
                                                                                       557 CTGACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCC 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Jane Massey Licata, Esq.
STREET: Woodland Falls Corporate Park
STREET: 210 Lake Drive East, Suite 20
CITY: Cherry Hill
                                                                                                                                                                                                                                                                  TYPE: NUCLEIC STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/464,954A FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAAGGGAAGAAACAGGCCCAGATCCTGGCCTCCGAAGCAGAAA 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGAGAGATGCTGACATTGGCGTGGCCGAGGCTGAACGGGACGCAGGCATCCGGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGGAAACGGGCCACAGTTCTAGAGTCTGAGGGGACCCGAGAGTCGGCCATCAATGTGGC 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGACGTGTATGACAAAGTGGACTATCTGAGCTCCCTGGGCAAGACGCAGACTGCCGTGGT 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATATCCATGTGCCACCCCGGGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCG 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Jane Massey Licata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                          Conservative
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                                                                                                                                         3.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JEFFREY L.; GOMEZ, JORGE; KUNAPULI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KINASES GRK5 AND GRK6
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                                                                                                                          Score 39.2; DB 4;
Pred. No. 0.16;
0; Mismatches 49;
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                                                                                                                                                           Length 2557;
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1377 GCGGCCGTAAGGAGAAGGTGAAGCGGGAGGAGGTGGACCGCCGGGTCCTGGAGACGG 1433

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; NAME/KEY:
; LOCATION:
US-08-221-817-12
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US-08-454-439-12
Sequence 12, Application US/08454439
Patent No. 5591618
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/123,932
FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532151and, Greta E.
REGISTRATION UMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Chicago
CITY: Chicago
TATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
                                                                                                                                                                                               1127
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                                                                                                                          1187
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                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                   557 CTGACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCC 616
                                                                                                                                                           617 GGGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IE
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                        AGCAGAGGAAGAAGAAGATCAAGCGGGAAGGAGGTGGAGCGGCTG 1230
                                                                                                                                                                                             CTGACTGGTGGGCGCTCGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCC 1186
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                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                 Score 39; DB 1; Length 2204; Pred. No. 0.17; 0; Mismatches 41; Indels
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; Sequence 12, Application PC/TUS9410487
; GENERAL INFORMATION:
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Best Local Similarity
Matches 63; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 31-MAR-1994
APPLICATION UMBER: 08/123
FILING DATE: 17 SEP 1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                     1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: NO. 5591618and, Greta
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 30-MAY-19
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                     1127 CTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCC 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2204 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: cDNA
                                              APPLICANT: ICOS COR
TITLE OF INVENTION:
TITLE OF INVENTION:
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                CORRESPONDENCE ADDRESS:
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STREET: 63
                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                     617 GGGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGG 660
                                                                                                                                                                                                                                                                                          557 CTGACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCC 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                   60606
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6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (312) 474-0448
                                                                                ICOS Corporation
                                                                                                                                                                                                                                                                                                                                            Conservative
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Marshall,
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                                Kinase GRK6
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                                                                 A Novel G Protein-Coupled Receptor
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O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greta E.
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                                                                                                                                                                                                                                                                                                                                          Score 39; DB Pred. No. 0.17 O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                              .17;
                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                Length 2204;
                                                                                                                                                                                                                                                                                                                                              Indels
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6300 Sears Tower, 233 South Wacker Drive

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RESULT 8
US-08-221-817-10
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                                                                                                                                                                                                              Sequence 10, Application US/08221817 Patent No. 5532151
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                GENERAL INFORMATION:
                                                                  APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: HoekStra, Merle F.
TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                        1187 AGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGAGCGGCTG 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          1127 CTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCC 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,
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                                                                                                                                                                                                                                                                                                                                                         617 GGGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                               557 CTGACTGCGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCC 616
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STREET: 6300 Sea:
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/2 FILING DATE: 31 MAR 1994 CLASSIFICATION:
                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/1: FILING DATE: 17 SEP 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
Chicago
                6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
                                                                                                                                                                                                                                                                                                                                                         660
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US-08-454-439-10
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; LOCATION:
US-08-221-817-10
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Appli
Patent No. 5591618
                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION UNMBER: 08/123
APPLICATION UNMBER: 1993
TOTAL DATE: 17 SEP 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATE: 17 SET TORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5532151and, Greta
NAME: NO. 1532151and, Greta
NAME: NO. 3532151and, Greta
NAME: NO. 5532151and, Greta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2206 base pairs
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1184 AGCAGAGGAAGAAGATCAAGCGGGAGGAGGTGGAGCGGCTG 1227
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APPLICATION NUMBER: US/08/221,817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 557 CTGACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCC 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    617 GGGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGG 660
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COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                        STREET: 6300 S
                                                                                                                     COUNTRY:
                                                                                                                                          STATE:
                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                   60606
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                                                                                                                                                                            6300 Sears Tower, 233 South Wacker Drive
                                                                                                                     USA
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    PatentIn Release #1.0,
                                                                                                                                                                                                   Borun
                                                                                                                                                                                                                   Marshall, O'Toole, Gerstein, Murray
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    Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US

FILING DATE:

30-MAY-1995

US/08/454,439

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/123, JAPPLICATION NUMBER: 08/123, JAPPLICATION NUMBER: 08/123, JAPPLICATION NAME: 1 STATEMENT NUMBER: 08/123, JAPPLICATION NUMBER: 08/123,
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: CLICAGO
CITY: Chicago
CITY: Illinois
TRATE: III
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                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1184 AGCAGAGGAAGAAGAAGATCAAGCGGGGAGGAGGTGGAGCGGCTG 1227
                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 31 MAR 1994
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LENGTH: 2206 base pairs
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PRIOR APPLICATION DATA:
US 08/221,817
                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: A Novel G Protein-Coupled Receptor TITLE OF INVENTION: Kinase GRK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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CLASSIFICATION
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                                                                                                                                CLASSIFICATION:
                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: · 60606
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31..1926
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Pred. No. 0.17;
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RESULT 11
US-08-149-097D-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23, Application US/08149097D
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1124 CTGACTGGTGGGCGCTCGGCTGCCTCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCC 1183
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
             APPLICATION NUMBER: 08/11 FILING DATE: 11-AUG-1993 PRIOR APPLICATION DATA:
                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                             SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1184 AGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGAGCGGCTG 1227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Noland, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Brenner, Robert TITLE OF INVENTION: HUMAN CONTITLE OF INVENTION: METHODS NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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CLASSIFICATION:
                                                                                              APPLICATION NUMBER: FILING DATE: 05-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Noland, Greta E. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                 CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 60.6 es 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                 92101-2926
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                                                                                                                                                                                                                                                                California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2206 base pairs
                                                                                                                                                                                                                                                                                             E: Brown, Martin, Haller & McClain
1660 Union Street
                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                               Williams, Mark
Feldman, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ellis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harpold, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                 McCue, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                05-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.3%;
                                                                                                                                                                                                                                                                                                                                                                                HUMAN CALCIUM CHANNEL COMPOSITIONS AND
                                                                                                                                                                                                                                                                                                                                                                  METHODS
                                                 08/105,536
                                                                                                                                                Release #1.0,
                                                                                                               US/08/149,097D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/123,932
WO PCT/US92/06903
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Pred. No. 0.17;
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                                                                                                                                                Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
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APPLICATION NUMBER:

US 07/914,231

APPLICATION DATA: DATE:

14-AUG-1992

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RESULT 12
US-08-949-386-23
Sequence 23, Application US/08949386
; Patent No. 6090623
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INFORMATION FOR SEQ ID NO: 23
SEQUENCE CHARACTERISTICS:
LENGTH: 7791 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 111; Conserv
GENERAL INFORMATION:
                                                                                                                         2513 CATGTCTATAGCTGTGAAAGAGCAACAGAAGAATCAAAAGCCAAGCCAAGTCC
                                                                                                                                                                                              2453 GAAACTTGCCCTACAGAAAGCCAAGGAGGTGGCAGAAGTGAGTCCTCTGTCCGCGGCCAA 2512
                                                                                                                                                                                                                                                                      2393 CGCCCAGGAGCTCACCAAGGTGGAGGCGACGAGCAAGAAGAAGAAGCAGCGAACCA 2452
                                                                                                                                                                                                                                                                                                                                             2333 CTTTGGGAACTACACCCTCCTGAATGTGTTCTTGGCCATCGCTGTGGACAATCTGGCCAA 2392
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: WO PO FILING DATE: 04-APR-1989 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07
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                                                                                                                                                                                                                                                                                                                                                                    564 CTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGGTGAA 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                            744 GGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCC 795
                                                                                                                                                                                                                                                                                                         624 AGAGTCTATGCAGATGCAGGTGGAGGCCAGAGCGGCGGAAACGGGCCACAGTTCTAGAGTC 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 240..7037
OTHER INFORMATION: /product= "Alphala-2 subunit of
OTHER INFORMATION: human calcium channel"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Seidman, Stephanie L. REGISTRATION NUMBER: 33,779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 10-API
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                                                                                                                                                                                                                                  TGAGGGGACCCGAGAGTCGGCCATCAATGTGGCAGAAGGGAAGAAACAGGCCCAGATCCT 743
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-APR-1988
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47.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB Pred. No. 0.31
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
0.31;
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                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                              2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: APPLICANT:
2513 CATGTCTATAGCTGTGAAAAGAGCAACAGAAGAATCAAAAAGCCAAGCCAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 11-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 11-AUG-1994
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MEDIUM TYPE: Floppy disk
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APPLICANT:
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                               744 GGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCC 795
                                                                                                                                                                          624 AGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAGAGTC 683
                                                                                                                                                                                                                                 564 CTGGGGTATCCGCTGCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGGTGAA 623
                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 237..703
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
NAME/KEY: CDS
NAME/KEY: CDS
NAME/KEY: CDS
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FILING DATE: 5-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                    TGAGGGGACCCGAGAGTCGGCCATCAATGTGGCAGAAGGGAAGAAACAGGCCCAGATCCT 743
                                                                                                                                                                                                            CTTTGGGAACTACACCCTCCTGAATGTGTTCTTGGCCATCGCTGTGGACAATCTGGCCAA
                                                                     GAAAACTTGCCCTACAGAAAAGCCAAGGAGGTGGCAGAAGTGAGTCCTCTGTCCGCGGCCAA 2512
                                                                                                                                       CGCCCAGGAGCTCACCAAGGTGGAGGCGACGACGAGCAAGAAGAAGAAGCAGCGAACCA 2452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1660 Union Street
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Ellis, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double
                                                                                                                                                                                                                                                                                                 3.3%;
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: 38
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                                                                                                                                                                                                                                                                                                                                                                                     /standard_name= "Alpha-1A-2"
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                                                                                                                                                                                                                                                                                                  Score 39; DB 3 Pred. No. 0.31;
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                                                                                                                                                                                                                                                                                Mismatches
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US-08-450-562-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404
FILING DATE: 13-MAR-1995
APPLICATION NUMBER: 08/331
FILING DATE: 7-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/914,231
FILING DATE: 13-JULY-1992
                                                                                 APPLICATION NUMBER: PCT/
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
                                                                                                                                  FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       FILING DATE: 07-FEB-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 5-NOV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/2
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                   PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 07/6
                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/10 FILING DATE: 11-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/31
FILING DATE: 23-SEPT-1994
                                                   APPLICATION NUMBER: 07/7 FILING DATE: 15-AUG-1991
                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/1 FILING DATE: 07-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/314,083 FILING DATE: 28-SEPT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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WENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
WENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gillespie, Alison
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Ellis, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                               4-APR-1994
                                                                                                                                                                                                                                                                                                            5-NOV-1993
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US-08-984-709A-23
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; OTHER INFORMATION:
US-08-450-562-23
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 7791 base pairs
LENGTH: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                    Sequence 23, Applicat: Patent No. 6320032 GENERAL INFORMATION:
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Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                      APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2333
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/1
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                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 6362-519812
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
COMPUTER READABLE FORM:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            744 GGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCC 795
                                                    STREET: 4250 Execu
CITY: La Jolla
STATE: California
                                      COUNTRY:
                                                                                            ADDRESSEE: Heller Ehrman White & McAuliffe STREET: 4250 Executive Square, Suite 700
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LOCATION: 237..7037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAACTTGCCCTACAGAAAGCCAAGGAGGTGGCAGAAGTGAGTCCTCTGTCCGCGGCCAA 2512
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                      92037
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NO: 23:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.3%;
47.8%;
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0.31;
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US-08-149-097D-22
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Best Local Similarity
Matches 111; Conserv
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NAME: Seidman, Stephanie L.
REGISTRATION UNMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
TELEPAX: (619) 587-5360
INFORMATION FOR SEQ ID NO: 23:
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LENGTH: 7791 base pairs
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                                                                                                                                                                         APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2333 CTTTGGGAACTACACCCTCCTGAATGTGTTCTTGGCCATCGCTGGGACAATCTGGCCAA 2392
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                        2513 CATGTCTATAGCTGTGAAAGAGCAACAGAAGAATCAAAAGCCCAGCCAAGTCC 2564
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                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 237..703
OTHER INFORMATION:
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COMPUTER: I
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STRANDEDNESS: double
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                                        ZIP:
                                                 COUNTRY:
                                                                        STATE:
                                                                                       CITY: San Diego
                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAACTTGCCCTACAGAAAGCCAAGGAGGTGGCAGAAGTGAGTCCTCTGTCCGCGGCCAA 2512
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                                      92101-2926
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                                                                       California
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                                                                                                       1660 Union Street
                                                                                                                                                                                                                                           Williams, Mark
Feldman, Daniel
                                                      USA
                                                                                                                                                                                                                              McCue, Ann
                                                                                                                                                                                                                                                                               Harpold, Michael
Ellis, Steven
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                                                                                                                      Brown, Martin, Haller & McClain
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02-DEC-1997
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 121;
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US-08-149-097D-22
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Best Local Similarity 47.8%;
Matches 111; Conservative
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: WO POFILING DATE: 04-APR-1989 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                       2393 CGCCCAGGAGCTCACCAAGGTGGAGGCGGACGAGCAAGAAGAAGAAGAAGCAGCGAACCA 2452
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                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                              624
                                                                                                                                                       564 CTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGGTGAA 623
684 TGAGGGGACCCGAGAGTCCGCCATCATGTGGCAGAAGGGAAGAAAACAGGCCCAGATCCT 743
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                                                                                                                                                                                                                                                                                                                       LOCATION: 240..776
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                            AGAGTCTATGCAGATGCAGGTGGAGGCAGAGCCGGCGGAAACGGGCCACAGTTCTAGAGTC 683
                                                                                                                                CTTTGGGAACTACACCCTCCTGAATGTGTTCTTGGCCATCGCTGTGGACAATCTGGCCAA 2392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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Search completed: September 22, 2002, 15:22:50 Job time: 6995 sec

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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCTTCTGGGAGCNACCGCT.........GGAAGCAGATTTTCCTGATT 1188
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cgn2_6/ptodata/1/pna/US6004_COMB.seq:*
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73 /cgn2_6/ptodata/1/pna/US6030_COMB.seq;
74 /cgn2_6/ptodata/1/pna/US6030_COMB.seq;
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79 /cgn2_6/ptodata/1/pna/US6030_COMB.seq;
79 /cgn2_6/ptodata/1/pna/US6030_COMB.seq;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Query Score Match Length DB

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	sequence 941, App sequence 941, App sequence 7309, Ap sequence 7358, Ap sequence 7925, Ap sequence 7914, App sequence 7917, Ap sequence 7917, Ap sequence 7917, Ap sequence 45, App1 sequence 45, App1 sequence 244, App sequence 249, App sequence 34, App1 sequence 34, App1 sequence 34, App1 sequence 3468, Ap sequence 347, App1 sequence 347, App1 sequence 3483, App sequence 3483, App sequence 3483, App sequence 3483, App	102, Ap 106, 1 1001, 1 2212, 1 865, 1 8410,

299

242

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REGISTRATION NUMBER: 36,373
REGISTRATION NUMBER: 92,008Complete
REFERNCE/DOCKET NUMBER: PZ008Complete
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8504
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 1322 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
PCT-US98-12125-102
Sequence 102, Application PC/TUS9812125
GENERAL INFORMATION:
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                                                                                   Query Match
Best Local S
Matches 1177
                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READDALE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4
COMPUTER: HP Vectta 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION NUMBER: PCT/US98/12125
FILING DATE: Jan 01, 1900
CLASSIFICATION:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
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FILING DATE:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION NUMBER:
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TITLE OF INVENTION: 86 Human Secreted Proteins
NUMBER OF SEQUENCES: 318
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61
                                                                                    Local Similarity
nes 1177; Conserv
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                                                    CTTCTGGGAGCNACCGCTCCGCTCGTCTCGTTGGTTCCGGAGGTCGCTGCGGCGGGGGA
AATGCTGGCGCGCGCGCGC - GNGGCACTGGGGCCCTTTTGCTGAGGGGCTCTCTACTGG
                                         CTTCTGGGAGCGACCGCTCCGCTCGTCTCGTTGGTTCCGGAGGTCGCTGCGGCGGTGGGA
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19 US-09-724-497-35

17 US-09-359-922-11863

17 US-09-359-922-11863

17 US-09-359-922-11863

18 US-60-360-207-118511

18 US-09-818-134-349

17 US-10-033-356-349

17 US-10-1155-213-1569

18 US-09-991-378-18015

19 US-09-991-378-18015

19 US-09-991-378-18015

10 US-09-991-378-18015

10 US-09-991-378-18015

10 US-09-991-378-18015

11 US-09-991-378-18015

12 US-09-991-378-18015

13 US-09-991-378-18015

14 US-09-991-378-18015

15 US-09-991-378-18015

17 US-10-066-543-2995
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Pred. No. 8.1e
1; Mismatches
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1es 7;
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Sequence 11863, A
Sequence 11863, A
Sequence 11863, A
Sequence 5097, Ap
Sequence 18511, A
Sequence 349, App
Sequence 1369, Ap
Sequence 11615, A
Sequence 11615, A
Sequence 11615, A
Sequence 11611, Ap
Sequence 2995, Ap
                                                                                    ۲.
                                                                                    Gaps
                   122
                                                              62
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APPLICANT: Hyseq, Inc.

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVel Nucleic Acids and Pol

FILE REFERENCE: 21272-030

CURRENT APPLICATION NUMBER: PCT/US01/03800A

CURRENT FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: 09/560,875

PRIOR APPLICATION NUMBER: 09/496,914

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SOFTWARE: Custom

SEQ ID NO 1001

LENGTH: 1398

TYPE: DNA

ORGANISM: Homo sapiens

PCT-US01-03800A-1001
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PCT-US01-03800A-1001/c
Sequence 1001, Application
GENERAL INFORMATION:
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RESULT 4

PCT-USO1-04098A-2212/c

PCT-USO104098A - 2212, Application PC/TUSO104098A

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-029

CURRENT APPLICATION NUMBER: PCT/USO1/04098A

CURRENT FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: Not Yet Assigned

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ORGANISM: Homo sapiens
-US01-04098A-2212
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OR APPLICATION NUMBER: 09/728,422
OR FILING DATE: 2000-11-30
OR APPLICATION NUMBER: 09/693,325
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 09/663,561
OR APPLICATION NUMBER: 09/654,936
OR APPLICATION NUMBER: 09/524,936
OR FILING DATE: 2000-09-01
OR APPLICATION NUMBER: 09/520,325
OR FILING DATE: 2000-07-19
OR APPLICATION NUMBER: 09/598,075
OR FILING DATE: 2000-06-20
OR APPLICATION NUMBER: 09/590,075
OR APPLICATION NUMBER: 09/590,075
OR APPLICATION NUMBER: 09/560,875
OR APPLICATION NUMBER: 09/560,875
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                                                                                           CAAACTCTCTNTGGACAAAGTCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGA
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FR APPLICATION NUMBER: US 60 FR FILING DATE: 1999-03-26 FR APPLICATION NUMBER: US 09 FR FILING DATE: 1999-05-07 FR APPLICATION NUMBER: US 09 FR APPLICATION NUMBER: US 09 FR APPLICATION NUMBER: US 09 FR FILING DATE: 1999-09-21 FR FILING DATE: 1999-09-21 FR FILING DATE: 1999-09-21

09/306 60/126, 60/125,

09/399 09/404

APPLICATION NUMBER: US (FILING DATE: 1999-03-19

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; Sequence 865, Application
; GENERAL INFORMATION:
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVel
TITLE OF INVENTION: NOVel
TITLE OF INVENTION: From V
FILE REFERENCE: 782
CURRENT FILING DATE: 1999-
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ER FILING DATE: 1999-01-22
ER APPLICATION NUMBER: US 09/240,3:
ER FILING DATE: 1999-01-9
ER APPLICATION NUMBER: US 09/277,2:
ER FILING DATE: 1999-03-25
ER APPLICATION NUMBER: US 09/271,4:
ER FILING DATE: 1999-03-18
ER FILING DATE: 1999-03-18
ER FILING DATE: 1999-03-18
ER APPLICATION NUMBER: US 09/293,9:
ER APPLICATION NUMBER: US 09/274,8:
ER FILING DATE: 1999-03-23
ER FILING DATE: 1999-03-23
ER FILING DATE: 1999-03-23
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NUMBER OF SEQ ID NOS: 10451
SOFTWARE: pt_CT_genes Version 1
SEQ ID NO 865
LENGTH: 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 1182; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1398
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1296)...(264)
OTHER INFORMATION: similar to 912984585 in the genepept database release
OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
-09-471-275-865
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                                                                      GAAACGGGCCACAGTTCTAGAGTCTGAGGGGACCCGAGAGTCGGCCATCAATGTGGCAGA 719
                                                                                                                CAAACTCTCTNTGGACAAAGTCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGA
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                              AGGGAAGAACAGGCCCAGATCCTGGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCA
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GGCAGCAGGAGAGGCCAGTGCAGTTCTGGCGAAGGCCAAGGCTAAAGCTGAAGCTTATTCG
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Pred. No. 2.6e
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                             CCAGGGTACAGATGCAAGTCTTGATGAGGAACTTGATCGAGTCAAGATGAGTTAGTGGAG
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RESULT 6
US-09-496-914A-8410/c
Sequence 8410, Application US/09496914A
GENERAL INFORMATION:
APPLICANT: Tang, Yuanhua T.
APPLICANT: Tang, Yuanhua T.
APPLICANT: Tillinghast, John
APPLICANT: Sinku, Ankura
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NOVEL Contigs Obtained
TITLE OF INVENTION: NOVEL CONTIGS Obtained
TITLE PRILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/353,690
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 09/045,400
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 09/045,400
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR APPLICATION NUMBER: US 09/321,517
PRIOR APPLICATION NUMBER: US 09/321,517
PRIOR APPLICATION NUMBER: US 09/31,517
PRIOR APPLICATION NUMBER: US 09/32,782
PRIOR APPLICATION NUMBER: US 09/332,782
PRIOR APPLICATION NUMBER: US 09/346,956
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PRIOR APPLICATION NUMBER: US 60/125,453

PRIOR FILING DATE: 1999-03-19

PRIOR FILING DATE: 1999-03-26

PRIOR PPLICATION NUMBER: US 60/126,605

PRIOR APPLICATION NUMBER: US 09/306,350

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: US 09/399,720

PRIOR FILING DATE: 1999-09-21

PRIOR APPLICATION NUMBER: US 09/404,284

PRIOR FILING DATE: 1999-09-21

PRIOR APPLICATION NUMBER: US 09/404,284

PRIOR FILING DATE: 1999-09-12

PRIOR APPLICATION NUMBER: US 09/465,877

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: NOT YET ASSIGNED PRIOR FILING DATE: 1999-11-19

PRIOR FILING DATE: 1999-01-19

NUMBER OF SEQ ID NOS: 10410

SOFTWARE: Dt CT Genes Version 1.02
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Best Local Similarity
Matches 1182; Conserv
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SEQ ID NO 8410
LENGTH: 1398
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OTHER INFORMATION: similar to gi2984585 in the genepept database
OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
-09-496-914A-8410
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FEATURE:
NAME/KEY: misc_feature
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OR FILING DATE: 1999-03-23
OR APPLICATION NUMBER: US 60/125,453
OR FILING DATE: 1999-03-19
OR APPLICATION NUMBER: US 60/126,605
OR FILING DATE: 1999-03-26
OR APPLICATION NUMBER: US 09/306,350
OR FILING DATE: 1999-05-07
OR FILING DATE: 1999-05-07
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                                                                                          CAAACTCTCTNTGGACAAAGTCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGA
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1296)...(264)
; OTHER INFORMATION: similar to gi2984585 in the genepept databa;
; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-560-875A-8410
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US-09-560-875A-8410/c
S-69uence 8410, Application US/09560875A
GENERAL INFORMATION:
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                                                                                                         Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 10410
SOFTWARE: pt_CT_genes Version 1.02
SEQ ID NO 8410
LENGTH: 1398
                                                                                                                                                                                                   APPLICANT: Tillinghast, John
APPLICANT: Sinku, Ankura
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 787
                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/560,875A CURRENT FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                     APPLICANT: Tang, Yuanhua T.
APPLICANT: Tillinghast, John
                                                                                              LENGTH: 13
TYPE: DNA
                                                                                 ORGANISM: Homo sapiens
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Query Match Best Local Similarity

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Score Pred.

1160; No. 2

DB 22; .6e-278;

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                                                                                     AATCCTGGCTGCAGCTCTGACACAACATAATGGAGATGCAGCAGCŤTCACTGACTGTGGC
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                                 CTCCAACCCTGGCGATGTCACCAGCATGGTGGCTCAGGCCATGGG
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APPLICANT: Holtzman, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DEI
TITLE OF INVENTION: HUMAN PROSTATE STROMAL LII
FILE REFERENCE: MLN98-25p
CURRENT APPLICATION NUMBER: US/09/338,467
CURRENT FILING DATE: 1999-06-22
EARLIER APPLICATION NUMBER: 60/090,177
EARLIER APPLICATION NUMBER: 60/090,177
RENTING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 1022
NUMBER OF SEG ID NOS: 1022
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 941
LENGTH: 1384
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                        tctctctggacaaagtcttccgggaacgggagtccctgaatgccagcattgtggatgcca
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Pred. No. 4.5e-277;
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                                                                                              CURRENT APPLICATION NUMBER: US/09/644,869
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,062
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9708
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8024
LENGTH: 1384
                                                                                                                                                                                                                                                                           Sequence 8024, Application US/09644869 GENERAL INFORMATION:
           Query Match
Best Local Similarity
Matches 1177; Conserv
                                                                  ORGANISM: HOMO
-09-644-869-8024
                                                                                                                                                                                      APPLICANT: Holtzman, Douglas A. APPLICANT: Monahan, John APPLICANT: Richardson, Jennifer TITLE OF INVENTION: NOVEL NUCLEIC TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.1182-001
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                                                                                      TYPE: DNA
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           Conservative
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                     97.2%;
99.4%;
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                     Score 1155;
Pred. No. 4
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APPLICANT: Shyjan, Andrew w.
APPLICANT: Richardson, Jennifer
APPLICANT: Holtzman, Douglas A.
ITITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFOR
ITILE REFERENCE: 1600.1181-001
CURRENT APPLICATION NUMBER: US/09/649,162
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,057
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9990
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7309
LENGTH: 1384
TYPE: DNA
ORGANISM: Homo sapiens
US-09-649-162-7309
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US-09-649-162-7309
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Matches 1177
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Pred. No. 4.5e-277;
O; Mismatches 5;
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SEQ ID NO 7925
LENGTH: 1384
TYPE: DNA
ORGANISM: Homo S
US-09-652-109-7925
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APPLICANT: MCCarthy, Sean A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MC
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1180-001
CURRENT APPLICATION NUMBER: US/09/652,109
CURRENT FILING DATE: 2000-08-30
                                                                                                        Query Match
Best Local Similarity
Matches 1177; Conserv
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                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/: PRIOR FILING DATE: 1999-08-30
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 GCTGGCGCGCGCGGCGGGGGCACTGGGGCCCTTTTGCTGAGGGGCTCTCTACTGGCTT 125
                                                    CTGGGAGCNACCGCTCCGCTCGTCTCGTTGGTTCCGGAGGTCGCTGCGGCGGTGGGAAAT 65
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                                 ctgggagcgaccgctccgctcgtctcgttggttccggaggtcgctgcggcggtgggaaat 63
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Pred. No. 4.5e-277;
D; Mismatches 5;
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GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: MOVEL NUCLEIC
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1183-001
CURRENT APPLICATION NUMBER: US/09/0
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,1
PRIOR APPLICATION NUMBER: 60/151,1
PRIOR TILING DATE: 1999-08-30
PRIOR FILING DATE: 1999-08-30
VMMBER OF SEQ ID NOS: 10475
SOFTWARE: FastSEQ for Windows Vers
SEQ ID NO 7358
LENGTH: 1384
TYPE: DNA
ORGANISM: Homo sapiens
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                               atgtgccaccccgggtgaaagagtctatgcagatgcaggtggaggcagagcggcagaaac
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APPLICANT: Gutlerrez-Ramos, Jose-Carlos
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES ANI
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 1600.117-001
: CURRENT APPLICATION NUMBER: US/09/652,816
: CURRENT FILING DATE: 2000-08-31
: PRIOR APPLICATION NUMBER: 60/152,111
: PRIOR APPLICATION NUMBER: 60/152,111
: PRIOR FILING DATE: 1999-08-31
: NUMBER OF SEQ ID NOS: 9647
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 7419
: LENGTH: 1384
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GENERAL INFORMATION:
APPLICANT: Gutter
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TYPE: DNA
ORGANISM: HOMO
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gtacagatgcaagtcttgatgaggaacttgatcgagtcaagatgagttagtggagctggg
                                    GTACAGATGCAAGTNITGATGAGGAACTTGATCGAGTCAAGATGAGTTAGTGGAGCTGGG
                                                        ACCCTGGCGATGTCACCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTCACCA
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RESULT 14 US-09-652-913-8809 ; Sequence 8809, Application US/09652913 ; GENERAL INFORMATION:

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SOFTWARE: FastSEQ fo.
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Best Local Similarity
Matches 1177; Conserv
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ORGANISM: HOMO
-09-652-913-8809
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CURRENT APPLICATION NUMBER: US/09/652,913
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,107
PRIOR FILING DATE: 1999-08-31
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TITLE OF INVENTION: HORNEL NUCLEIC ACID MOLECULES
TITLE OF INVENTION: THERREFOR
FILE REFERENCE: 1600:1174-001
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Pred. No. 4.5e-277;
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLE
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1193-001
CURRENT APPLICATION NUMBER: US/09/652,914
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 06/152,112
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9677
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7997
LENGTH: 1384
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US-09-652-914-7997
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APPLICANT: Shyjan, Andrew
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Best Local Similarity
Matches 1177; Conserv
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         CTTNGCCAGGGAGTCTGGGGACAAGGAAGCAGATTTTCCCTGATT 1188
                                                GTACAGATGCAAGTNTTGATGAGGAACTTGATCGAGTCAAGATGAGTTAGTGGAGCTGGG 1144
                                                                            AAGCCCCAGTGCCAGGGACTCCAGACTCACTCTCCAGTGGGAGCAGCAGAGATGTCCAGG 1084
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                                     gtacagatgcaagtcttgatgaggaacttgatcgagtcaagatgagttagtggagctggg
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Search completed: Job time: 6835 sec September 22, 2002, 16:14:40

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US-09-705-256A-3468
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US-09-19-018-846-13409
PCT-US01-43704-1161
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US-09-629-469A-1950
PCT-US01-43704-1175
US-10-146-502-193
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37, Appl
11863, Ap
11963, Ap
1197, Appl
1950, Appl
1951, Appl
1953, Appl
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12975, A
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	Sequence 18465, A	Sequence 29396, A	Sequence 7770, Ap	Sequence 8142, Ap	Sequence 15714, A	Sequence 30091, A	Sequence 688, App	Sequence 2445, Ap	Sequence 26126, A	Sequence 4825, Ap	Sequence 14079, A	Sequence 17868, A	Sequence 37723, A	Sequence 28244, A	Sequence 21791, A	Sequence 8693, Ap	Sequence 9558, Ap	Sequence 6734, Ap	Sequence 26, Appl	Sequence 26, Appl

ALIGNMENTS

SEQUENCE DESCRIPTION: SEQ ID NO: US-09-898-216-2 US-09-898-216-2 RESULT Sequence 2, Application US/09898216 GENERAL INFORMATION: TELEX: <Unknown> INFORMATION FOR SEQ ID NO: 2: COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ for Windows Version 2. CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/898,216 FILLING DATE: 02-Jul-2001 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/781,562 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS: ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166 SEQUENCE CHARACTERISTICS: IMMEDIATE SOURCE: APPLICANT: Hillman, Jennifer L. STATE: CA COUNTRY: USA ZIP: 94304 LENGTH: 1188 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear REFERENCE/DOCKET NUMBER: PF-0181 US CITY: Palo Alto LIBRARY: Consensus Surya K. <u>د</u>

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Match Local Similarity

Length 1188;

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                    TCCAACCCTGGCGATGTCACCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTC
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APPLICANT: ROSEON et al.

APPLICANT: ROSEON et al.

FILE REFERENCE: PZ008D1C1

CURRENT FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: 09/209, 462

PRIOR FILING DATE: 1998-06-11

PRIOR APPLICATION NUMBER: 60/049, 547

PRIOR FILING DATE: 1997-06-13

PRIOR APPLICATION NUMBER: 60/049, 549

PRIOR APPLICATION NUMBER: 60/049, 549

PRIOR APPLICATION NUMBER: 60/049, 549

PRIOR FILING DATE: 1997-06-13

PRIOR APPLICATION NUMBER: 60/049, 566

PRIOR FILING DATE: 1997-06-13

PRIOR APPLICATION NUMBER: 60/049, 606

PRIOR FILING DATE: 1997-06-13

PRIOR APPLICATION NUMBER: 60/049, 606

PRIOR APPLICATION NUMBER: 60/049, 607

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PRIOR APPLICATION NUMBER: 60/049, 607

PRIOR FILING DATE: 1997-06-13

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PRIOR APPLICATION NUMBER: 60/049, 611

PRIOR FILING DATE: 1997-06-13

PRIOR APPLICATION NUMBER: 60/050, 901

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PRIOR APPLICATION NUMBER: 60/050, 901

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PRIOR APPLICATION NUMBER: 60/050, 901

PRIOR APPLICATION NUMBER: 60/050, 901

PRIOR APPLICATION NUMBER: 60/050, 966

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PRIOR APPLICATION NUMBER: 60/050, 966

PRIOR APPLICATION NUMBER: 60/050, 966

PRIOR APPLICATION NUMBER: 60/050, 969

PRIOR APPLICATION NUMBER: 60/050, 972

PRIOR APPLICATION NUMBER: 60/050, 975

PRIOR APPLICATION NUMBER: 60/060, 834

PRIOR APPLICATION NUMBER: 60/060, 834

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Best Local Similarity
Matches 1177; Conserv
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NAME/KEY: SITE
LOCATION: (1322)
OTHER INFORMATION: (10-219-793-106
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SEQ ID NO 106
LENGTH: 1322
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PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,059
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,060
PRIOR FILING DATE: 1997-10-02
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FILING DATE: 1997-10-02
APPLICATION NUMBER: 60/060,865
FILING DATE: 1997-10-02
             ACTCTCTNTGGACAAAGTCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGC
                                                                      GGACCCTGAGTATGCCGTCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCAA 482
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; NAME/KBY: misc_feature
; LOCATION: 1, 2, 1909, 19
; OTHER INFORMATION: n = A
US-10-198-846-12975
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                                                                                                                                           SOFTWARE: FastSEQ for Windows SEQ ID NO 12975
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GENERAL INFORMATION:
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                           LENGTH: 1910
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          CCAACCCTGGCGATGTCACCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTCA
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                                                ageagtatgteagegetteteeaaaetggeeaaggaeteeaaeaetateetaetgeeet
                                                             AGCAGTATGTCAGCGCGTTCTCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCCT
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Pred. No. 1.1e
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APPLICANT: MONABAN, JOHN
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PRI
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PRI
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/201,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/219,007
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; LOCATION: 1841, 1842
; OTHER INFORMATION: n =
US-09-785-276A-24973
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 24973
LENGTH: 1842
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Best Local Similarity
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TYPE: DNA
ORGANISM: Homo:
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TGGAGCCTGGTTTGAACATCCTCATCCCTGTGTTAGACCGGATCCGATATGTGCAGAGTC
                                                         tgttcgtgccgcagcaggaggcctgggtggtggagcgaatgggccgattccaccggatcc
                                                                              TGTTCGTGCCGCAGCAGGAGGCCTGGGTGGTGGAGCGAATGGGCCGATTCCACCGGATCC
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Pred. No. 5.46
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Sequence 45, Application US/10219793
GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: 86 Human Secreted Protei
FILE REFERENCE: P2008P1C1
CURRENT APPLICATION UNMBER: US/10/219,793
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/209,462
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(OR APPLICATION NUMBER: 60/049,609

FOR FILING DATE: 1997-06-13

FOR APPLICATION NUMBER: 60/049,610

FOR FILING DATE: 1997-06-13

FOR APPLICATION NUMBER: 60/050,901

FOR APPLICATION NUMBER: 60/050,901

FOR APPLICATION NUMBER: 60/052,989

FOR APPLICATION NUMBER: 60/052,989

FOR APPLICATION NUMBER: 60/051,919

FOR APPLICATION NUMBER: 60/051,919

FOR FILING DATE: 1997-06-13

FOR APPLICATION NUMBER: 60/055,984

FOR APPLICATION NUMBER: 60/058,665

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APPLICANT: OTSURI, TETSUJI

TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FUI

FILE REFERENCE: 08435/0123

CURRENT APPLICATION NUMBER: US/09/629,469A

CURRENT FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: JP 1999-248036

PRIOR FILING DATE: 1999-07-29

PRIOR FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: JP 2000-118776

PRIOR APPLICATION NUMBER: JP 2000-183767

PRIOR APPLICATION NUMBER: JP 2000-183767

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: JP 2000-241899

PRIOR APPLICATION NUMBER: JP 2000-241899

PRIOR APPLICATION NUMBER: 60/159,590

PRIOR APPLICATION NUMBER: 60/159,590

PRIOR FILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/159,590

PRIOR APPLICATION NUMBER: 60/183,322

PRIOR FILING DATE: 2000-02-17

NUMBER: DATE: 2000-02-17

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APPLICANT: ISOCAL, TAKA
APPLICANT: HAYASHI, KOJ
APPLICANT: SAITO, KAORU
APPLICANT: YAMAMOTO, JU
APPLICANT: ISHII, SHIZU
  Query Match
Best Local Similarity
Matches 1153; Conserv
                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver.
SEQ ID NO 11009
LENGTH: 1244
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                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                FEATURE:
                                                                                                                                                                                 ORGANISM: Homo
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YAMAMOTO, JUNICHI
ISHII, SHIZUKO
SUGIYAMA, TOMOYASU
WAKAMATSU, AI
WAKAMATSU, KEIICHI
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99.4%;
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Score 1130.4;
Pred. No. 3.9e
0; Mismatches
4; DB 5;
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                                              aacttgatcgagtcaagatgagttagtggagctgggcttggccagggagtctggggacaa
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; NAME/KEY: CDS
; LOCATION: (75)..(9098)
US-10-119-428-37
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US-10-119-428-37
Sequence 37, Application US/10119428
GENERAL INFORMATION:
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TITLE OF INVENTION: NOVel Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 789CIP2
CURRENT APPLICATION NUMBER: US/10/119,42
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 5000-05-19
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Best Local Similarity
Matches 1128; Conserv
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                                                                              gttcgtgccgcagcaggaggcctgggtggtggagcgaatgggccgattccaccggatcct
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                gcaaatcgatggagtcctttacctgcgcatcatggacccttacaaggcaagctacggtgt
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Ma, Yunqing
Zhou, Ping
Zhao, Qing A.
Yang, Yonghong
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hrman, Tom
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Pred. No. 1.7
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APPLICANT: Ma, Xiao-Jun; Dotson, Stanton B.: Mon:
TITLE OF INVENTION: Tumor Associated Molecules (TI
TITLE OF INVENTION: and prevention of cancer
FILE REFERENCE: 3214
CURRENT APPLICATION NUMBER: US/09/705,256A
CURRENT FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: US 60/164,285
PRIOR APPLICATION NUMBER: US 60/164,285
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 8259
SEQ ID NO 3468
LENGTH: 1234
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US-09-705-256A-3468
; Sequence 3468, App
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            Query Match
Best Local Similarity
Matches 1131; Conserv
                                                               TYPE: DNA
ORGANISM: Homo:
-09-705-256A-3468
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                                                             CTGACTGTGGCCGAGCAGTATGTCAGCGCGTTCTCCAAACTGGCCAAGGACTCCAACACT
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                     agcagagatgtccagggtacagatgcaagtcttgatgaggaacttgatcgagtcaagatg
                               AGCAGAGATGTCCAGGGTACAGATGCAAGTNTTGATGAGGAACTTTGATCGAGTCAAGATG
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PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US
PRIOR FILING DATE: FILING DATE: 1998-02-13
NUMBER OF SEO ID NOS: 13203
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11863
LENGTH: 1309
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Best Local
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APPLICANT: Liu, Jin
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-752CON1
CURRENT APPLICATION NUMBER: US/09/919,002
CURRENT FILING DATE: 2001-075
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ORGANISM: Homo sapiens
-09-919-002-11863
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                     GTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCCATGTG-CCACCCCGGGTGAAAGAG
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PRIOR APPLICATION NUMBER: 60/306,220 PRIOR FILING DATE: 2001-07-18 NUMBER OF SEQ ID NOS: 14084 SOFTWARE: FastSEQ for Windows Version 4 SEQ ID NO 13409 LENGTH: 1150 TYPE: DNA PRESENTED NA SEQUENCY OF SECULAR SEQUENCY OF SECULAR SECULAR SEQUENCY OF SECULAR    Дb
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: THERAPY OF BREAST, CANCER
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CURRENT FILING DATE: 2002-07-18
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                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1149, 1150
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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Local Similarity
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97.9%;
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Pred. No. 1.8e-196;
0; Mismatches 13;
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RESULT 11

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SEQUENCE 1161, APPLIC

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corixa CC
APPLICANT: Stolk,
APPLICANT: Chenault
APPLICANT: Meagher,
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 2101
CURRENT APPLICATION
CURRENT APPLICATION
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS
SOFTWARE: COrixa Inv
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 APPLICANT: Corixa Corporation
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Su, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCI
FILE REFERENCE: 210121.561PC
CURRENT APPLICATION NUMBER: PCT/US01/43704
CURRENT APPLICATION NUMBER: PCT/US01/43704
CURRENT FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Databa:
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Sequence 2995, Application U.
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Chenault, Ruth,
APPLICANT: Xu, Jiangchun
APPLICANT: Indirias, Carol.
APPLICANT: Lodes, Michael,
APPLICANT: Secrist, Heathe,
APPLICANT: Carter, Darrick
APPLICANT: Smith, Carole L
APPLICANT: Smith, Carole L

Indirias, Carol Yoseph Ruth

Lodes, Michael J.
Secrist, Heather
Carter, Darrick
Fanger, Gary R.
Smith, Carole L.

RESULT 12 US-10-214-403-2995/c

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LENGTH: 622
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
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OTHER INFORMATION: n = 1
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Best Local S
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CAGGCCCAGATCCTGGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGA
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Pred. No. 1.1e-146;
1; Mismatches 3;
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/10/214,403
CURRENT FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 3420
SOFTWARE: FFastSEQ for Windows Version 4.0
SEQ ID NO 2995
LENGTH: 550
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 411
OTHER INFORMATION: n = A,T,C or G
US-10-214-403-2995
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PCT-US01-43704-58
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                                               Sequence 58, Application PC/TUS0143704 GENERAL INFORMATION:
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Best Local Similarity
Matches 547; Conserv
APPLICANT:
         APPLICANT: Corixa Corporation APPLICANT: Stolk, John A. APPLICANT: Xu, Jiangchun
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                                                                                                                           TGTCCAGGGT
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APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR T
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561PC
CURRENT APPLICATION NUMBER: PCT/US01/43704
CURRENT FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: COTIXA INVENTION Disclosure Database
SEQ ID NO 58
LENGTH: 563
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TYPE: DNA
ORGANISM: Homo s
PCT-US01-43704-58
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Sequence 1428, Application US/10097105
GENERAL INFORMATION:
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Best Local S
           APPLICANT: Meagher, Madeleine Joy
APPLICANT: King, Gordon E.
APPLICANT: Secrist, Heather
APPLICANT: Harlocker, Susan L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCE
FILE REFERENCE: 210121.504C1
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 APPLICATION
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 NUMBER:
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99.3%;
US/10/097,105
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| LENGTH: 691
| TYPE: DNA
| ORGANISM: Homo saplens
| FEATURE:
| NAME/KEY: misc_feature
| LOCATION: 439, 508, 523, 526, 539, 56
| LOCATION: 626, 645, 648, 664
| OTHER INFORMATION: n = A,T,C or G
| US-10-097-105-1428
RESULT 15
US-09-629-469A-1950
; Sequence 1950, Application US/09629469A
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
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NUMBER OF SEQ ID NOS: 1562
SOFTWARE: FBSTSEQ for Windows Version
SEQ ID NO 1428
LENGTH: 691
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Best Local Similarity
Matches 616; Conserv
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Pred. No. 7.4e-121;
0; Mismatches 46;
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CURRENT APPLICATION NUMBER: US/09/629,469A
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: JP 1999-248036
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 1999-300253
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR APPLICATION NUMBER: 60/159,590
PRIOR FILING DATE: 1999-10-18
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SEQ ID NO 1950
LENGTH: 567
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TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEIR USE
FILE REFERENCE: 084335/0123
                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (508)..(508)
OTHER INFORMATION: "n"
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ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (533)..(533)
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NAME/KEY: misc_feature
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Best Local Similarity 97.0
Matches 550; Conservative
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ALIGNMENTS

2 (bases 1 to 1218)
Ye,M., Zhang,Q.H., Zhou,J., Shen,Y., Wu,X.Y., Guan,Z.Q., Wang,L., Fan,H.Y., Mao,Y.F., Dai,M., Huang,Q.H., Chen,S.J. and Chen,Z. Human full length cDNA cloned from cd34+ stem cells Unpublished
3 (bases 1 to 1999) Submitted (23-JUN-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II, Shanghai 200025, P. R. China, Location/Qualifiers
1. .1218 Ye,M., Zhang,Q.H., Zhou,J., Fan,H.Y., Mao,Y.F., Dai,M., for 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells Genome Res. 10 (10), 1546-1560 (2000) Zhang,Q.H., Ye,M., Wu,X.Y., Ren,S.X., Zhao,M., Zhao,C.J., Fu,G., Shen,Y., Fan,H.Y., Lu,G., Zhong,M., Xu,X.R., Han,Z.G., Zhang,J.W., Tao,J., Huang,Q.H., Zhou,J., Hu,G.X., Gu,J., Chen,S.J. and Chen,Z. Cloning and functional analysis of cDNAs with open reading frames Homo sapiens HSPC108 mRNA, complete Direct Submission Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AF161458.1 (bases 1 to 1218) (bases 1 to 1218) /clone="CBCAPB12"
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                             GCCGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACACAACA 866
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    TAATGCAGATGCAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGTTCTCCAA
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KAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLA
KDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTTPDSLSSGSSRDVQGTDASLDE
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Pred. No. 1.7; Transition 7;
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             GCAGCAGGAGGCCTGGGTGGTGGAGCGAATGGGCCGGATTCCACCGGATCCTGGAGCCTGG 248
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AL541792
AL541792.1 GI:12
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1 (bases 1 to 935)
Li,W.B., Gruber,C., Jessee,J.
Full-length cDNA libraries and
Unpublished (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BP 191 91006 EVRY cedex - France
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                                                      Conservative
                                                                                                                                    /organism="Homo sapiens"
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139 a 246 c 265 g 181 t 4 others
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Location/Qualifiers
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                          BM476304
AGENCOURT_6479118 N
5', mRNA sequence.
BM476304
BM476304.1 GI:1852
Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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NIH_MGC_88
Chordata;
Primates;
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Craniata; Vertebrata; Catarrhini; Hominidae
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MAGE:5558923
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Plate: LLAM12282 row: k column: 20
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High quality sequence stop: 678
Location/Qualifiers
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Tissue Procurement: ATCC
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Unpublished (1999)
Contact: Robert Strausberg,
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/db_xref="taxon:9606"
/clone="IMAGE:5558923"
/clone_lib="NHLMGC_88"
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/lab_host="DH108 (phage-resistant)"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_1: NotI: Site_2: SalI; Cloned unidirectionally;
Oligo-dT prined. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
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Genoscope - Centre National
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Full-length cDNA libraries
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(bases 1 to 962)
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         /note-*Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life the normalized libraries.
                                                                                                     /clone="CSODA006YH04"
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                                                                               /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
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fliang@lifetech.com URL:
http://fulllength.invitrogen.com*
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Email: cgapbs-r@mail.nih.gov
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/Clone=lib="NIH_MGC_72"
/Lissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
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Tissue Procurement: ATCC/DCTD/DTP
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                       AGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACACAACATAATGGAGATGCAGCAGC
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/clone="imAGE:5578.33"
/clone_lib="wilh MCC_72"
/tissue_type="melanotic melanoma"
/lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Si
/note="Organ: skin; Vector: pCMV-SPORT6; Si
/site_2: Sall; Cloned unidirectionally. Pri
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RS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Shiraki, T., Tanaka, T., Tejima, Y., Toya, T., Yamanaka, I., Yasahishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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Mus musculus (strain:C57BL/6J) adult male kidney cDNA to clone_lib:RIKEN full-length enriched mouse cDNA library
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Encyclopedia Project of Genome Exploration
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/clone_lib="RIKEN full-length enriched mouse
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/strain="C57BL/6J"
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Pred. No. 1.7e-195;
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               BM461614.1
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                                               BM461614
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CDNA linear :DNA clone

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                                                     CCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCAAACTCTGTUTGGACAAAGTCT
                              GCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGT
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Plate: LLAM12137 row: n column: 16
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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/db_xref="Taxon:9666"
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/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
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/note="Organ: eye; Vector: pCMV-SPO@T6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.75 kb. Library constructed by
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AL525168.1
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1 (bases 1 to 849)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage
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          195
/tissue_type="neuroblastoma cells"
//tissue_type="neuroblastoma cells"
/lab_host="DH108"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6; 1st stranded with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
1 others
                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cS0DC005YF20"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
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ans cDNA clone CS0DC005YF20 5
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Query Match
Best Local Similarity
Matches 844; Conserv

Conservative

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69.1%; 99.3%;

Score 821.4; Pred. No. 1.5e 0; Mismatches

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849;

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AGENCOURT_6387825 NIH_MGC_71 H;
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Primates;
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Hominidae;
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          Euteleostomi;
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• IMAGE:5529785
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                                                                    AGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACACAACATAATGGAGATGCAGCAGC
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                                                      AGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACACAACATAATGGAGATGCAGCAGC
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NH+MGC http://mgc.nci.nih.gov/.
NAtional Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ATCC
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="InAGE:5529785"
/clone="lib="NxH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DHHOB (phage-resistant)"
/nab_host="DHHOB (phage-resistant)"
/note="organ: uterus; Vector: pCMV-SPORT6; Si-Site_2: Sali; Cloned unidirectionally. Prime Average insert size 2.1 kb. "
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Genoscope - Centre National de Sequencage
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Full-length cDNA libraries
Unpublished (2001)
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Mammalia; Eutheria;
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                                                                                                                                                                                       175
                                                                                     Conservative
                                                                                                                                                                                /tissue_type="neuroblastoma cells"
//lab_host="0H10B"
//lab_host="19H10B"
//note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6]
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/clone_lib="LTI_NFL003_NBC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
                                                                                                67.6%;
94.2%;
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Primates;
                                                                                  Score 802.6;
Pred. No. 6.3e
24; Mismatches
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Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 1095)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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AGENCOURT_6402181 NIH_MGC_41
5', mRNA sequence.
BM423347
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MAGE:5516467
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                                                                                                                                                   GCTGGGGTATCCGCTGCCTCCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGGTGA
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TGGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCCCAGTGCAG
                                                                                          TCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: LLCM2017 row: b column: High quality sequence stop: 503.
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/tlosue_type="amelanomtic melanoma, cell line"
/tissue_type="amelanotic melanoma, cell line"
/tlab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5 adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NH_MGC Library."

85 a 282 c 302 g 226 t
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/clone="IMAGE:5516467"
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Contact: Robert Strausberg, Ph.D.
                                                               Similarity 97.; 36; Conservative
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Tissue Procurement: ATCC
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//note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 2.1 kb. "
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 ATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGGTGAAAGAGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: AFCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (1
DNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLCM1430 row: e column: 15
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61; Conservative
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//tissue_type="choriocarcinoma"
/lab_host="PHIOB (phage resistant)"
/note="Organ: placenta; vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 254 c 290 g 189 t
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/db_xref="taxon:9606"
/clone="IMAGE:4649846"
/clone_lib="NIH_MGC_21"
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98.4%;
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O; Mismatches
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Indels Length

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GTCCTTTACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAG 432
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                                                                                       804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 920)
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/clone_lib="NIH_MCC_87"
/clone_lib="NIH_MCC_87"
/tissue_type="mammary defenocarcinoma, cell line"
/tissue_type="mammary def
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/db_xref="taxon:9606"
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                                                                                 Score 791.2; DB Pred. No. 4e-183; 0; Mismatches
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TGCAAGTNTTGATGAGGAACTTGATCGAGTCAAGATGAGTTAGTGGAGCTGGGCTTNGCC
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                                          TGCCAGTCTTGATGAGGAACTTGATCGAGTCAAGATGAGTTAGTGGAGCTGGGCCTTGGCC
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Search completed: September 22, 2002, 14:49:21 Job time: 5287 sec

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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DUS6_HUMAN
DUS6_MOUSE
 ZUO1_YEAST
MDHP_SPIOL
TBA4_HUMAN
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CARBOHYD 160 160
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STRAIN-LONG EVANS; TISSUE-Lung;

JONES M.L., Shanley T.P., Ward P.A.;

JONES M.L., Shanley T.P., Ward P.A.;

Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T

CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE F

BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Secreted.
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P16756;
01-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-90269039; PubMed-2161319; Chee M.S., Bankler A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddle E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.; "Analysis of the protein-cooling content of the sequence of human cytomegalovirus strain AD169.";
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                Rattus norvegicus (Rat).
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Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
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SUBCELLULAR LOCATION: Secre SIMILARITY: BELONGS TO THE C-C) (CHEMOKINE CC).
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Sciurognathi; Muridae; Murinae; Rattus
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Rhodospirillum.
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                                                              entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Falk G., Hampe A., Walker J.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Falk G., Hampe A., Walker J.E.;
Nucleotide sequence of the Rhodospirillum
Biochem. J. 228:391-407(1985).
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SIMILARITY: BELONGS TO THE ATPASE EPSILON CHAIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Produces ATP from ADP in gradient across the membrane. CATALYTIC ACTIVITY: ATP + H(2)O +
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                                                                                    http://www.isb-sib
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RL29_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDIJNR-96180309; PubMed-8597591;

Law P.T., Tsui S.K., Lam W.Y., Luk S.C., Hwang D.M., Liew C.C.,

Lee C.Y., Fung K.P., Waye M.M.;

"A novel cDNA encoding a human homologue of ribosomal protein L29.";

Biochim. Biophys. Acta 1305:105-108(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPL29
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Pfam; PF02823; ATP-synt_DE, 1.
ProDom; PD000944; ATP-synt_DE; 1.
Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport.
SEQUENCE 134 AA; 14307 MW; 8905084DF31C9222 CRC64;
                                                                                                                                                      ProDom; PD
Ribosomal
                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96216099; PubMed=8662616;
Liu S., Smith S.E., Julian J., Rohde L.H., Karin "cDNA cloning and expression of HIP, a novel cell sulfate/heparin-binding protein of human uterine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Law P.T.W., Tsui S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
60S_ribosomal protein L29 (Cell surface heparin binding protein HIP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                  [NIT_MET
                                                                                                                                                                                                    Pfam; PF01779; Ribosomal_L29e;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229
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                                                                                                                                                                                                                       nterPro; IPR002673; Ribosomal_L29e.
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SIMILARITY: BELONGS TO THE L29E FAMILY OF RIBOSOMAL PROTEINS
19083; An.,
11832; -
12902673; Ribosoma.
129e; 1.
129e; 1
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rohde L.H., Karin N.J., Carson D.D
HIP, a novel cell surface heparan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waye M.M.Y.;
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                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collaboration
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RESULT RESULT REPORTED TO THE PORT OF THE 
  RESULT 7

K2C5_BOVIN

ID K2C5_B

AC P04262

DT 20-MAR

DT 20-MAR

DT 16-OCT
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Best Local
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Q9K6D6;
16-0CT-2001 (Rel. 40, C
16-0CT-2001 (Rel. 40, L
16-0CT-2001 (Rel. 40, L
K2C5_BOVIN
P04262;
20-MAR-1987
20-MAR-1987
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                halodurans and genomic sequence comparison with Bacillus subtilis.";

Nucleic Acids Res. 28:4317-4331(2000).

-I- FUNCTION: PARTICIPATES IN BOTH THE INITIATION AND RECYCLING PHASES

OF TRANSCRIPTION. IN THE PRESENCE OF THE DELTA SUBUNIT, RNAP

DISPLAYS AN INCREASED SPECIFICITY OF TRANSCRIPTION, A DECREASED

AFFINITY FOR NUCLEIC ACIDS, AND AN INCREASED EFFICIENCY OF RNA

SYNTHESIS BECAUSE OF ENHANCED RECYCLING (BY SIMILARITY).

-I- SUBUNIT: RNAP IS COMPOSED OF A CORE OF 2 ALPHA, A BETA AND A

BETA' SUBUNITS. THE CORE IS ASSOCIATED WITH A DELTA SUBUNITS AND

ONE OF SEVERAL SIGNA FACTORS (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO THE RPOE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Takami H., Nakasone K., Takaki Y., Maeno G.
Fuji F., Hirama C., Nakamura Y., Ogasawara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus halodurans.
Bacteria; Firmicutes; Bacteria; Firmicutes; Bacillus/Staphylococcus
NCBI_TaxID=86665;
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RPOE OR BH3793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Complete genome sequence of the alkaliphilic bacterium Bacillus
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104 164. I
64 AA; 19213 MW;
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RNA polymerase delta
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Pred. No.
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ASP/GLU-RICH (ACIDIC).
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                                                                                               PRT;
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delta subunit (RNAP delta
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P76471;
15-DEC-1998
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SEQUENCE
                     SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A., (
                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001664; IF. Pfam; PF00038; filament; 1. PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-85128114; PubMed-6084625;
Jorcano J.L., Franz J.K., Franke W.W.;
"Amino acid sequence diversity between bovine epidermal cytokeratin
polypeptides of the basic (type II) subfamily as determined from cDi
clones.";
                                                                                                                                                          YFAZ OR B225
                                                                                                                                                                                15-DEC-1998
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; K03534; AAA30601.1; -. PIR; A02948; KRBO2B. HSSP; P10968; IWGC.
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Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                       Escherichia
                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                            Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Intermediate filament; Coiled coil; Keratin.
                                                                                                                                                                                                                                                                                            145
                                                                                                                                                                                                                                                                                                                  331 LSSGSSR 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restress by non-profit institutions as long as its content ified and this statement is not removed. Usage by and
            B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFIBRILLAR KERATIN, I (ACIDIC) AND II (NEUTRAL TO BASIC)
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complete
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(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
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166
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Ruminantia; Pe
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                       Goeden
                                Rode C.K., Mayhew
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K-12.";
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yhew G.F.,
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RESULT 9
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                                                                                             modified and this statement is not removed, entities requires a license agreement (See or send an email to license@isb-sib.ch).
          InterPro; IPR002639; UreF.
Pfam; PF01730; UreF; 1.
ProDom; PD004961; UreF; 1.
                                                      EMBL; U32736;
TIGR; HI0537;
                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                 Science 269:496-512(1995).
-!- FUNCTION: PROBABLY FACILITATES NICKEL INCORPORATION
-!- SIMILARITY: BELONGS TO THE UREF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; P.
Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN*RD / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae
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                                                                                                                                                                                                                                                                                         Venter J.C
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P57066;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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_VIBCH
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STRAIN=EL TOR N16961 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOLD OR VC1883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE004263; AAF95031.1; -. TIGR; VC1883; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                           ATP-binding; Transport; Complete proteome.

NP_BIND 41 48 ATP (BY SIMILARITY).

SEQUENCE 228 AA; 24890 MW; 315E52CB775E61E6 CRC64;
                                                                                                                                                                                                                                                                                                                                    SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_tra
InterPro; IPR001687; ATP_GTI
InterPro; IPR0005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                   249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOR THE RELEASE OF LIPOPROTEINS TARGETED TO THE OUTER MEMBRANE FROM THE INNER MEMBRANE. SUCH A RELEASE IS DEPENDENT OF THE SORTING-SIGNAL (ABSENCE OF AN ASP AT POSITION 2 OF THE MATURE LIPOPROTEIN) AND OF LOLA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVAQAMG
                               AKAKAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        releasing
                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BELONGS TO THE ABC TRANSPORTER FAMILY. LOLD SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40,
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                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEROTYPE 01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inner membrane-associated (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                     Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B38F134AE3DCD0B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                         Mismatches
                                                                                                                  No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO.
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27;
                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                  Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
FIXA_RHILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 01-FEB-1995 
                                                                                                                                                                                                                                                                                                                                                                                              FIXA_RHILP
Q05559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _BACHD
                                                                                                                                                                               Rhizobium leguminosarum (biovar phaseoli).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   halodurans and genomic sequence comparison with Bacil Nucleic Acids Res. 28:4317-4331(2000).
-!- FUNCTION: INVOLVED IN DNA REPAIR (BY SIMILARITY).
Michiels J.,
                                                                                                                                                  Bacteria; Proteobacteria; Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD007415; RadC; 1 PROSITE; PS01302; RADC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00633; HHH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000445; HHH. InterPro; IPR001405; RadC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP001517; BAB06751.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takami H., Nakasone K., Takaki Y., Maeno G., S
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus/Staphylococcus
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RADC OR BH3032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA repair protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RADC_BACHD
                            MEDLINE=93379046; PubMed=8369342;
                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE RADC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 SLNASIV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by non-profit institutions as long
                                                                                                                                                                                                                                                                        protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLNASIV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKAKAKA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 100 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete
Vanderleyden
                                                                                                                                               Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JCM 9153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                 . 31, Created)
. 31, Last sequence of the sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40, Created)
40, Last sequence up
40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 radC
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26403 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.0%;
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                                                                                                                                                                                                                                                                                                     Last sequence update)
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., Kuhara S.,
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P19654;
O1-FEB-1991
O1-FEB-1991
O1-FEB-1991
                                                                                                                                                            Sternberg N., Cohen G.;
"Genetic analysis of the lytic replicon of bacteriophage Pl. II.
Organization of replicon elements.";
J. Mol. Biol. 207:111-133(1989)
-I- FUNCTION: ESSENTIAL FOR L-REPLICON FUNCTION. NECESSARY FOR
INITIATION OF DNA REPLICATION FROM THE L-REPLICON (PROBABLE).
   EMBL;
                 EMBL;
                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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Pfam; PF01012; ETF_beta; 1.
ProDom; PD003528; ETF_beta; 1.
PROSITE; PS01065; ETF_BETA; 1.
Electron transport; Nitrogen fixation
Electron transport; Nitrogen fixation
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                                                                                                                                                                                                                                                           MEDLINE=89293846; PubMed=2661830,
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                       Structure and regulation of the lytic replicon of Mol. Biol. 207:135-149(1989).
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X15639; CAA336562.1;
X15638; CAA33656.1;
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                            viruses, no
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                                                                                    rmatics Institute. There are no resi
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A ROLE IN A REDOX PROCESS INVOLVED IN NITROGEN
                                                                                                                                                                                                                                                                                                                                                                                                            RNA stage; Caudovirales; Myoviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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RESULT 14
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Best Local
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15-JUL-1998
16-OCT-2001
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029013;
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                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus."; Nature 390:364-370(1997).
PRINTS; PR00100; AOTCASE.
PROSITS; PS00097; CARBAMOYLTRANSFERASE; FALSE_NEG.
PTRANSFERASE; Arginine biosynthesis; Complete proteome.
SEQUENCE 307 AA; 34913 MW; DB043BC5A40EBB5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X15638; CAA33657.1; ALT_INIT
PIR; S04263; RLEPP1.
DNA replication.
SEQUENCE 281 AA; 30857 MW; F3C:
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Archaea; Euryarchaeota;
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                                                                                             InterPro; IPR002029;
                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: ARGININE BIOSYNTHESIS (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter J.C.
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AF1255; -.
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36, Last sequence update)
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Search completed: September 22, Job time: 294 sec
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                                                                                                                                                Query Match 2.0%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 45; Matches 7; Conservative 0; Mismatches
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7_SPIOL
IN37_SPIOL
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                                                                                                                                                                                                                                 EMBL; X56963; CAA40283.1; -.
PIR; $14409; $14409.
InterPro; IPR000051; $AM_bind.
InterPro; IPR000051; $M_bind.
InterPro; IPR004033; ubit_COQ5_methyltransf.
Pfam; PF01209; Ubite_methyltran; 1.
Chloroplast; Transit_peptide; Inner membrane.
Chloroplast; Transit_peptide; Inner membrane.
TRANSIT 1 21 CHLOROPLAST.
CHAIN
22 344 37 KDA INNER ENVELOPE MEMBRANE PROTEIN.
SEQUENCE 344 AA; 38976 MW; 555E53242B297D7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "cDNA sequence and deduced amino acid sequence of the precursor of the 37-kDa inner envelope membrane polypeptide from spinach chloroplasts. Its transit peptide contains an amphiphilic alpha-helix as the only detectable structural element.";

Eur. J. Blochem. 195:361-368(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
37 kDa inner envelope metabrane protein, chloroplast precursor (E37).
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01-NOV-1991
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MEDLINE-91146572; Pubmed-1997321;
Dreses-Warringloer U., Fischer K., Wachter E., Link T.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     envelope protein.";
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MEDLINE-91348205; PubMed-1879527;
Block M.A. Joyard J., Douce R.;
"Purification and characterization of E37, a major chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            luegge U.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3562;
                                                                              154 LAKAKAK 160
                                                                                                      248 LAKAKAK 254
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SUBCELLULAR LOCATION: CHLOROPLAST INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287:167-170(1991).
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              2002, 18:37:12
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Maximum DB seq length: 2000000000
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Perfect score:
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                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 60.0 , Gapext 60.0
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T205863
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RESULT 2 T21562 Typothetical C;Species: CG C;Date: 15-00 C;Accession: R;Barlow, K. submitted too A;Reference to A;Reference to A;Accession: A;Accession: A;Status: pro A;Molecule typo	Qy 194 VE Db 195 VE Qy 254 KA P P P P P P P P P P P P P P P P P P	A; Introns: 2/ C; Superfamily Cuery Match Best Local	RESULT 1 T02246 hypothetical proteic: Homo sap C; Species: Homo sap C; Date: 05 Mar-1999 C; Accession: T02246 R; Lamerdin, J.E.; M; Christensen, M.; .; Christensen, M; Lamerdin, Sequ A; Authors: Duarte, A; Description: Sequ A; Reference number: A; Accession: T02246 A; Status: translate A; Molecule type: DN A; Residues: 1-357 A; Cross-references: C; Genetics:		3322 3322 3322 3322 3323 3323 3323 332
protein F aemorhabdi ct-1999 #s T21562 the EMBL number: Z1 T21562 eliminary;	EABERKRAITLESEGTRESAIN	y: erythrocyte y: erythrocyte h Similarity 52; Conservat	pin apie 99 ## 166 # 166 # 166 # 166 # 166 # 166 # 166 # 166 # 166 #		77 77 77 77 77 77 77 77 77 77 77 77 77
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Caenorh s vision ry, Oct	INVAEGKOAQI	7 integral 7 score 152 0; Pred. No	n 05 ror la, rch hum	ALIGNMENTS	A84124 KRBO2B S43815 C07795 H64995 B91021 B91021 F64865 F64865 F64865 F63148 F17794 J74683 J74683 B75372 C82556 ABD75372 H84028
abditis elegans 15-Oct-1999 #text_change 21-Jan-2000 ober 1996 GB/ЕмВL/DDBJ	VEAERKKAIVLESEGTRESAINVAEGKOAQILASEAEKAEQINQAAGEASAVLAKAKA 253	194/3; 243/1; 269/3; 312/3 11 membrane protein .52; DB 2; Length 357; NO. 4.9e-142; NO. 4.9e-142; natches 0; Indels 0; Gaps 0;	%-Mar-1999 #text_change 11-Jan-2000 sski, E.; Adamson, A.W.; Burkhart-Schultz, K. J.; Liu, S.; Attix, C.; Andreise, T.; Trank 1998 R.; Thomas, P.; Quan, G.; Kronmiller, B.; Ar nan Pl clone containing the XRCC9 DNA repair	MENTS	NA-directed RNA p keratin, 68K type hypothetical prote stage V sporulatio hypothetical prote hypothetical prote hypothetical prote hypothetical prote urease accessory p hypothetical prote hypothetical prote hypothetical prote T-cell receptor 9a hypothetical prote hypothetical prote conserved hypothet ABC transporter, A DNA repair protein

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C:Genetics:
A:Gene: Rp328
C:Superfamily: erythrocyte band 7 integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein T29A15.70 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 13-Aug-1999 C;Accession: T05863 R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volch submitted to the Protein Sequence Database, March 1999 A;Reference number; Z15455 A;Accession: T05863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-334 <WIL>
A; Cross-references: EMBL:Z81072; PIDN:CAB03018.1; GSPDB:GN00019; CESP:F30A10.5
A; Experimental source: clone F30A10
C; Genetics:
A; Gene: CESP:F30A10.5
A; Map position: 1
A; Introns: 16/2; 68/3; 124/3; 227/2
C; Superfamily: erythrocyte band 7 integral membrane protein
                                                                                                                                   A:Title: The genome sequence of Rickettsia prowazekii and the A:Reference number: A71630; MUID:99039499
A:Accession: B71689
A:Status: preliminary; nucleic acid sequence not shown; transl A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-311 < AND>
A:Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PI
A:Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-515 <BEV>
A;Cross-references: EMBL:AL035602
A;Experimental source: cultivar Columbia;
C;Genetics:
                                                                                                                                                                                                                                                                           C;Accession: B71689
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark,
Nature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                RESULT
B71689
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                                                                                                                                                                                                                                                                                                                         hypothetical protein RP328 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
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A; Introns: 52/2; 133/3;
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Matches 11
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Matches 13; Conservative
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   Local Similarity 100 hes 11; Conservative
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Pred. No.
                   Score 11;
Pred. No.
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Pred. No.
   Mismatches
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                   DB 2;
0.013;
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0.00021
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                                 Length 311
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   Indels
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                                                                                                                                                        PIDN:CAA14788.1;
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early protein p12 - phage PRD1
C;Species: phage PRD1
C;Date: 03-Aug-1990 #sequence_revision
C;Accession: A35148; JQ0186
R;Gerendasy, D.; Ito, J.
J. Bacteriol. 172, 1889-1898, 1990
                                                                                                                                                                                                                                                                                                                                              A; Map position: 2
A; Introns: 72/2; 265/2
C; Superfamily: erythrod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein SPBC16G5.07c - fissic;Species: Schizosaccharomyces pombe C;Date: 03-Dec1999 #sequence_revision 03-Dec-1999 C;Accession: T39599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: D97756

R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, Science 293, 2093-2098, 2001

A;Title: Mechanisms of Evolution in Rickettsia conorii al A;Reference number: A97700; MUID:21442074; PMID:11557893

A;Accession: D97756
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D97756
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-354 <LYN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Lyne, M.; Wood, V.; Rajandream, M.A.; submitted to the EMBL Data Library, May A;Reference number: Z21866
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AL023554; PIDN:CAA19027.1; GSPDB:GN00067; SPDB:SPBC16G5.07c A;Experimental source: strain 972h-; cosmid c16G5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: T39599
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C; Superfamily:
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A; Residues: 1-312 < KUR>
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C; Date: 30-Sep-2001
                                                                                                              A35148
                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: SPDB: SPBC16G5.07c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein RC0452 [imported] - Rickettsia conorii (strain Malish C;Species: Rickettsia conorii
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Best Local
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100.0%;
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Pred. No. 0.013;
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                                                      03-Aug-1990
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                                                                                                                                                                                                                                                                         DB 2;
0.014;
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                                                      #text_change
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A;Cross-references: 1
C;Genetics:
A;Map position: 3
A;Note: C0800w
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R;Lawson, D.; Bowman, S.; Barrell, B. submitted to the EMBL Data Library, August 1997
A;Reference number: Z18935
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M30146; NID:g215762; PIDN:AAA32453.1; PID:g215763 R;Pakula, T.M.; Savilahti, H.; Bamford, D.H.
Gene 85, 53-58, 1989
A;Title: The organization of the right-end early region of bacteriophage A;Reference number: JQ0186; MUID:90152379
A;Accession: JQ0186
A;Accession: JQ0186
A;Mccession: JQ0186
A;Residues: 1-160 <PAK>
A;Cross-references: GB:M33428; NID:g215747; PIDN:AAA32447.1; PID:g215748
C;Keywords: DNA binding
                                                                                                           R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon N. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: E87425
    A; Molecule type: DNA
A; Residues: 1-248 <STO>
A; Cross-references: GB:
C; Genetics:
                                                                                                                                                                                                                                                                                    transcription regulator, GntR family [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 30-Sep-2001 C;Accession: E87425
                                                                                                                                                                                                                                                                                                                                                                                     RESULT
E87425
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A; Residues: 1-374 <LAW>
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A; Residues: 1-160 <GER>
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Best Local S
Matches 9
                                                                                            Status: preliminary
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Best Local :
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9; Conserv
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9; Conserv
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                        GB:AE005673; NID:g13422783; PIDN:AAK23401.1; GSPDB:GN00148
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Query Match
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Query Match
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"-+~hes 8; Conserv:
F;1-25/Domain: signal sequence #status predicted <SIG>F;26-343/Product: hypothetical protein UL14 #status predicted F;281-305/Domain: transmembrane #status predicted crystal-305/Domain: transmembrane #status predicted crystal-305/Domain: transmembrane #status (Asn) (covalent) #status
                                                                                                                 A;Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35447.1; PID:g59619 A;Note: this sequence was submitted to the EMBL Data Library, December 1:C;Superfamily: human cytomegalovirus hypothetical protein UL14
                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-343 <CI
                                                                                                                                                                                                                                                   Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A; Fittle: Analysis of the protein-coding content of
A; Reference number: S09749; MUID:90269039
A; Accession: S09777
                                                                                                                                                                                                                                                                                                                                                                                              A;Note: host Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
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A;Molecule type: DNA
A;Residues: 1-263 <ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: G83163
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.;
                                                                                          C;Superfamily: human cytomegalovirus hypothetical protein
C;Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                           R;Chee, M.S.; Bar
M.; Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein UL14 precursor - human cytomegalovirus (strain AD169)
C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
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C;Superfamily: pyruvate dehydrogenase complex repressor
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                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S09777
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Best Local :
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8; Conserv
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100.0%; Pr
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Pred. No.
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Pred. No.
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    #status predicted
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                                                                                                                                        December 1989
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2.2%;

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Length

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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; L1, J.H.; L1, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: C96680
  В
                                    Ş
                                                                                                                                                                                                                                                                                                                                       A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Accession: AG3259

A;Streence namber: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: AG3259
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein BMEI0060 [imported] - Brucella melitensis (strain 16M) C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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A; Gene: F5I14.7
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                                                                                                                                                                                    A; Map position: I
                                                                                                                                                                                                                             A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Rosidues: 1-400 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL51242.1; PID:g17981931; GSPDB:GN00190
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                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                          Query Match 2.2%; Score 8; Best Local Similarity 100.0%; Pred. No. Matches 8; Conservative 0; Mismatc
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Best Local Similarity
Matches 8; Conserv
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PVPGTPDS 28
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ilarity 100.0%;
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Pred. No.
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T18801
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Query Match
Best Local Similarity
Change 8; Conserv
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                                                                                                                                                                                                                       A;Cross-references: GB:AE007870; PIDN:AAK89198.1; PID:g15159016; GSPDB:GN00170 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                         R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Gold A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                aldehyde dehydrogenase dhas [imported] - Agrobacterium tumefaciens (strain C58, Cereo C;Speciles: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002 C;Accession: D98209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Thes 8; Conserv
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A;Introns: 20/2; 49/2; 113/1; 169/1; 260/2; 375/3;
C;Superfamily: Caenorhabditis elegans hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:283245; PIDN:CAB05840.1; GSPDB:GN00020; CESP:ZK131.11 A;Experimental source: clone ZK131 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, A; Reference number: Z19024 A; Accession: T18801
                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-493 <KUR>
                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: D98209
                                                                                                                                                                                                                                                                                                                                                       A; Title: Genome Sequence of the Plant Pathogen and A; Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 C;Accession: T18801; T27746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein ZK131.11 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
                                                                                                                                                                                                A; Gene: AGR_L_1241
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A;Experimental source: clone C01B9
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A; Residues: 1-477 <WIL>
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253 AKAEAIRI 260
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ilarity 100.0%;
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100.0%;
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                                                                DB 2;
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                                                                                  Length 493
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Search completed: September 22, 2002, 18:32:59 Job time: 172 sec

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score
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/cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
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                            US-09-898-216-1
US-09-629-469A-11010
US-10-219-793-411
US-60-389-987-1904
US-60-389-987-768
US-60-389-987-768
US-60-389-987-68
US-10-219-793-416
US-10-219-793-422
US-10-219-793-422
US-10-219-793-424
US-10-219-793-417
US-10-219-793-417
US-10-219-793-417
US-10-219-793-417
US-10-219-793-417
US-10-219-793-412
US-10-219-793-413
US-10-219-793-427
US-10-219-793-427
US-10-219-793-425
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2441.243 Million cell updates/sec
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826, 1
768, 1
    51693,
   Query Match
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ALIGNMENTS

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US-09-898-216-1
US-09-898-216-1
US-09-898-216-1
Sequence 1, Application US/09898216
Sequence 1, Application US/09898216
Sequence 1, Application US/09898216
SEQUENCE 1NFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: HILLMan, Jennifer L.
APPLICANT: HILLMan, Jennifer L.
APPLICANT: HILLMan, Jennifer L.
APPLICATION NOVEL HUMAN MEMBRANE PROTEIN
MUMBER OF SEQUENCES: 7
CORRESSOR: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COUNTRY: USA
ZIP: 94304
COUNTRY: BALO Alto
STATE: CA
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: DISkette
COMPUTER SYSTEM: DOS
SOFTMARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/898,216
FILING DATE: CJ.ul-2001
CLASSIFICATION LUMBER: US/09/898,216
FILING DATE: CJ.ul-2001
CLASSIFICATION NUMBER: US/09/898,216
FILING DATE: CJNKNOWN>
APPLICATION NUMBER: 08/781,562
FILING DATE: CJNKNOWN>
APPLICATION NUMBER: 08/781,562
FILING DATE: GJNKNOWN>
APPLICATION NUMBER: 08/781,562
FILERENCE/DOCKET NUMBER: 36,749
RESERENCE/DOCKET NUMBER: BF-0181 US
TELEPHONE: 415-855-0555
TELEPAX: 415-854-4166
TELEX: CUNKNOWN>
INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-855-0555
TELEPAX: 415-854-4166
TELEX: CUNKNOWN>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
STRANDEDNESS: single
TOPOLOGY: Linear
IMMEDIATE SOURCE:
LENGTH: 356 amino acids
STRANDEDNESS: Single
TOPOLOGY: LINEARY: CONSENSUS
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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99.48;

Score 354;

DB 5;

Length 356;

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APPLICANT: NAGAI, KEITCHI
APPLICANT: ONSUKI, TETSUJI
TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FUI
FILE REFERENCE: 084335/0123
CURRENT APPLICATION NUMBER: U5/09/629,469A
CURRENT APPLICATION NUMBER: U5/09/629,469A
CURRENT FILING DATE: 2000-07-28
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: JP 1999-300253
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR APPLICATION NUMBER: G0/159,590
PRIOR APPLICATION NUMBER: 60/159,590
PRIOR FILING DATE: 1999-10-18
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US-09-629-469A-11010
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                                                                                   SOFTWARE: PATENTIN VET. 2
SEQ ID NO 11010
LENGTH: 356
TYPE: PRT
ORGANISM: Homo sapiens
US-09-629-469A-11010
Query Match
Best Local Sim
Matches 318;
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APPLICANT: ISOG
APPLICANT: NISH
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                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 19025
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                   Similarity
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ISHII, SHIZUKO
SUGIYAMA, TOMOYASU
WAKAMATSU, AI
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     Conservative
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Score 218; DE
Pred. No. 8e-1
0; Mismatches
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; Mismatches
               ; DB 5;
8e-197;
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CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/209,462
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: PCT/US98/12125
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/049,547
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR APPLICATION NUMBER: 60/049,549
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,549
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,549
PRIOR FILING DATE: 1997-06-13
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/049,550
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,566
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,606
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,607
PRIOR APPLICATION NUMBER: 60/049,607
PRIOR APPLICATION NUMBER: 60/049,607
PRIOR FILING DATE: 1997-06-13
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APPLICANT: Rosen et
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                                                                                                     PRIOR
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                                                                                                                                                                        PRIOR
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R APPLICATION NUMBER: 60/0
R FILING DATE: 1997-06-13
R PAPPLICATION NUMBER: 60/0
R FILING DATE: 1997-06-13
R APPLICATION NUMBER: 60/0
R FILING DATE: 1997-06-13
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FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/
                                                                 APPLICATION NUMBER: 60/055, FILING DATE: 1997-08-18
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/049,608 FILING DATE: 1997-06-13
APPLICATION FILING DATE:
                                 FILING DATE: 1997-09-12
                                                 APPLICATION NUMBER:
                                                                                                     FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/049,609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPG
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               NUMBER:
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                                                 60/058,665
                                                                                                                                                      60/052,989
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                 60/058,668
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RESULT 4
US-10-219-793-411
US-10-219-793-411
Sequence 411, Application US/10219793
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 86 Human Secreted Proteins
FILE REFERENCE: P2008p1C1
CURRENT APPLICATION NUMBER: US/10/219,793
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/209,462
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: PCT/US98/12125
PRIOR FILING DATE: 1998-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo
US-10-219-793-150
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LENGTH: 356
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Best Local Similarity
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FILING DATE: 1997-10-02
APPLICATION NUMBER: 60/060,865
FILING DATE: 1997-10-02
APPLICATION NUMBER: 60/061,059
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FILING DATE: 1997-10-02
APPLICATION NUMBER: 60/
FILING DATE: 1997-10-02
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FILING DATE: 1997-09-1
APPLICATION NUMBER: 60
FILING DATE: 1997-09-1
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APPLICATION NUMBER: 60/
FILING DATE: 1997-10-02
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99.7%;
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Pred. No. 8e-197;
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US-10-219-793-411
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PRIOR APPLICATION NUMBER: 60/058,975
PRIOR TILING DATE: 1997-09-12
PRIOR PELLING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/060,834
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/060,841
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/060,844
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
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PRIOR APPLICATION NUMBER: 60/058,665
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058,668
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058,669
PRIOR APPLICATION NUMBER: 60/058,669
PRIOR FILING DATE: 1997-09-12
                                                                                      SOFTWARE: PatentIn SEQ ID NO 411
                                                                                                                                  PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 737
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PRIOR APPLICATION NUMBER: 60/055,984
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PRIOR ALPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-66-13
PRIOR APPLICATION NUMBER: 60/
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PRIOR FILING DATE: 1997-06-1
PRIOR APPLICATION NUMBER: 60
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PRIOR APPLICATION NUMBER: 60
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PRIOR FILING DATE: 1997-10-02
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                                         LENGTH: 306
TYPE: PRT
                  ORGANISM: Homo sapiens
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APPLICATION NUMBER: 60/049,611
FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/050,901
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APPLICATION NUMBER: 60/049,609
EILING DATE: 1997-06-13
APPLICATION NUMBER: 60/049,610
EILING DATE: 1997-06-13
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Query Match
56.7%; Score 202; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 8.4e-182;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-389-987-1904
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TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465P2
CURRENT APPLICATION NUMBER: US/60/389,987
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: F881SEQ for Windows Version 4.0
SEQ ID NO 1904
                                                                                                                                                           Sequence 826, Application US/60389987 GENERAL INFORMATION:
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GENERAL INFORMATION:
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                                                                                                         APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibsón, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465P2
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                       ALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAP 323
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Taylor, Steven W.
Glenn, Gary M.
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CURRENT APPLICATION NUMBER: US/60/389,987
CCURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 826
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-60-389-987-826
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CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: EASTSEQ for Windows Version 4.0
SEQ ID NO 768
LENGTH: 342
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                                                                                                                                                                                                                                                                       Query Match 40.2%; Score 143; DB 7; L
Best Local Similarity 100.0%; Préd. No. 3.7e-126;
Matches 143; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenck, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 660088.465P2
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APPLICANT: Fahy, Eoin D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 VEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKA 254
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                323 PVPGTPDSLSSGSSRDVQGTDAS 345
                                                                                                          263 AALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKA 322
                                                                                                                                                                             189 TVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILA 248
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                                                                                       AALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKA
PVPGTPDSLSSGSSRDVQGTDAS 331
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RESULT 8 US-10-219-793-416 ; Sequence 416, Application US/10219793

INFORMATION

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; SEQ ID NO 416
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-793-416
                                                                                                                                     NUMBER OF SEQ ID NO SOFTWARE: Patentin
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CURRENT FILING DATE: 2002-08-16
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TITLE OF INVENTION: 86 Human Secreted Proteins
FILE REFERENCE: PZ008P1C1
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FILING DATE: 1997-06-13
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FILING DATE: 1997-10-02
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          OR FILING DATE: 1997-09-12
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OR FILING DATE: 1997-09-12
OR APPLICATION NUMBER: 60/060,834
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APPLICATION NUMBER:
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APPLICATION NUMBER:
FILING DATE: 1997-09
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60/060,844
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9.9e-47;
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PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,060
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 737
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 418
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CURRENT FILING DATE: 2002-08-16
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DR FILING DATE: 1997-06-13
DR FILING DATE: 1997-06-13
DR FILING DATE: 1997-06-13
DR APPLICATION NUMBER: 60/049,609
DR FILING DATE: 1997-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                 OR APPLICATION NUMBER: 60/049,550
R FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/049,566
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/049,606
R FILING DATE: 1997-06-13
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Local Similarity 100.0%; Pred. No. 9.9e-47;
Nes 58; Conservative 0; Mismatches 0;
  APPLICATION NUMBER: 60/058,668 FILING DATE: 1997-09-12
                                  APPLICATION NUMBER: 60/058,665 FILING DATE: 1997-09-12
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EILING DATE: 1997-06-13
APPLICATION NUMBER: 60/050,901
FILING DATE: 1997-06-13
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APPLICATION NUMBER: 60/060,865
FILING DATE: 1997-10-02
                                                                           FILING DATE: 1997-08-18
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RESULT 11
US-10-219-793-422
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CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/209,462
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: PCT/US98/12125
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/049,547
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR FILING DATE: 1997-06-13
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PRIOR FILLING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,550
PRIOR FILLING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,566
PRIOR APPLICATION NUMBER: 60/049,606
PRIOR FILLING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,606
PRIOR FILLING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,607
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SEQ ID NO 420
LENCTH: 50
TYPE: PRT
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Best Local Similarity 100.0%;
Matches 50; Conservative (
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PRIOR APPLICATION NUMBER: 60/049,609
PRIOR FILING DATE: 1997-06-13
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TITLE OF INVENTION:
FILE REFERENCE: PZOC
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PRIOR APPLICATION NUMBER: 60/060,865
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,059
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
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PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/060,834
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/060,841
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PRIOR APPLICATION NUMBER: 60/058,971
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058,972
PRIOR FILING DATE: 1997-09-12
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PRIOR APPLICATION NUMBER: 60/060,844
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APPLICATION NUMBER: 60/
FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/049,610 FILING DATE: 1997-06-13
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NVENTION: 86 Human Secreted Proteins
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Sequence 424, Application US/10219793

Sequence 424, Application US/10219793

GENERAL INFORMATION:
APPLICANT: Rosen et al.

FILL REFERENCE: PZ008P1C1

CURRENT APPLICATION NUMBER: US/10/219,793

CURRENT FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: 09/209,462

PRIOR FILING DATE: 1998-12-11

PRIOR FILING DATE: 1998-06-11

PRIOR APPLICATION NUMBER: 05/049,547

PRIOR APPLICATION NUMBER: 60/049,547

PRIOR APPLICATION NUMBER: 60/049,548

PRIOR FILING DATE: 1997-06-13
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Best Local
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TYPE: PRT
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FILING DATE: 1997-10-02
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FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/058,668
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FILING DATE: 1997-10-02
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FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/058,971
FILING DATE: 1997-09-12
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APPLICATION NUMBER:
FILING DATE: 1997-00
      FILING DATE: APPLICATION N
                      APPLICATION NUMBER: 60/049,549 FILING DATE: 1997-06-13
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FILING DATE: 1997-10-02
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llarity 100.0%; Pred. No. 1.4e-34;
Conservative 0; Mismatches 0;
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US-10-219-793-426
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                  Sequence 426, Application US/10219793
GENERAL INFORMATION:
APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Pa
SEQ ID NO 424
APPLICANT: Rosen et al.
TITLE OF INVENTION: 86 Human Secreted Proteins
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; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-793-424
                                                                       Query Match 12.6%; Score 45; DB Best Local Similarity 100.0%; Pred. No. 1. Matches 45; Conservative 0; Mismatches
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NUMBER OF SEQ ID NOS: 737
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APPLICATION NUMBER: 60/
FILING DATE: 1997-10-02
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FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/058,972
FILING DATE: 1997-09-12
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APPLICATION NUMBER: 60/058,975
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FILING DATE: 1997-06-13
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Best Local Similarity 100 Matches 35; Conservative

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Pred. No. 3.7e-25;
; Mismatches 0;

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; ORGANISM: Homo sapiens
US-10-219-793-426
                                                    NUMBER OF SEQ ID NOS: 737
SOFTWARE: PatentIn Ver. 2.
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CURRENT APPLICATION NUMBER: US/10/219,793
CURRENT FILING DATE: 2002-08-16
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APPLICATION NUMBER:
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FILING DATE: 1997-08-18
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FILING DATE: 1997-09-12
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FILING DATE: 1997-10-02
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FILING DATE: 1997-10-02
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Query Match

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RESULT 14
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APPLICANT: Rosen et
TITLE OF INVENTION:
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CURRENT APPLICATION NUMBER: US/10/219,793
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/209,462
PRIOR FILING DATE: 1998-12-11
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PRIOR FILING DATE: 1998-06-11
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DR APPLICATION NUMBER: 60/058,668
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DR APPLICATION NUMBER: 60/058,669
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DR APPLICATION NUMBER: 60/058,750
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DR APPLICATION NUMBER: 60/050,901
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DR APPLICATION NUMBER: 60/052,989
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DR APPLICATION NUMBER: 60/051,919
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APPLICATION NUMBER: 60/049,566
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APPLICATION NUMBER: 60/
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                   NUMBER: 60/060,865
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US-10-219-793-417
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PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 737
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 419
LENGTH: 30
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Matches 30; Conserv
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TITLE OF INVENTION: 86 Human Secreted Proteins
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PRIOR FILING DATE: 1997-10-02
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OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/049,611
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/050,901
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/052,989
OR APPLICATION NUMBER: 60/052,989
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/051,919
OR FILING DATE: 1997-07-08
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FILING DATE: 1997-06-13
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FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/058,665
FILING DATE: 1997-09-12
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                    FILING DATE: 1997-09-1
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PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR PRIOR APPLICATION NUMBER: 60/060,834
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
PRIOR PRIOR APPLICATION NUMBER: 60/060,841
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/060,864
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PRIOR APPLICATION NUMBER: 60/060,065
PRIOR APPLICATION NUMBER: 60/061,059
PRIOR APPLICATION NUMBER: 60/061,059
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,060
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,060
PRIOR FILING DATE: 1997-10-02
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PRIOR FILING DATE: 1997-10-02
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SEQ ID NO 417
LENGTH: 28
TYPE: PRT
                                                                                                             Matches
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Best Local Similarity 100.0%;
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Search completed: September 22, 2002, 18:35:49 Job time: 296 sec

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6 US-09-209-462B-150
PCT-US01-03800A-2351
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PCT-US01-04942A-222
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equence 57094	uence 428, Ap	equence 429. A	equence 5529,	equence 5433	e 5415	e 415,	276,	equence 425,	equence 423,	2 427,	equence 421,	e 4	e 412,	5	273,	e 413	274, Ap	equence 127	equence 2731	Sequence 417, App	equence 419,	equence 4903	4903	•	424,	422,	quence 598,	e 420,	equence 2934	equence 418,	equence 416,	1228,	ce 411,	272,	e 36,	e 36,	, App

ALIGNMENTS

RESULT 1 PCT-US98-12125-145

Sequence 145, Application PC/TUS9812125 GENERAL INFORMATION: APPLICANT: Rosen et al.

APPLICANT: Rosen et al.
TITLE OF INVENTION: 86 Human Secreted Proteins
NUMBER OF SEQUENCES: 318

CORRESPONDENCE ADDRESS:

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ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPB: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION NUMBER: PCT/US98/12125
FILING DATE: Jan 01, 1900
CLASSIFICATION:
APPLICATION NUMBER: PCT/US98/12125
FRICH APPLICATION NUMBER: FILING DATE:
APPLICATION NUMBER: PCT/US98/12125
FILING DATE: Jan 01, 1900
CLASSIFICATION NUMBER: PCT/US98/12125
APPLICATION NUMBER: PCT/US98/12125
REGISTRATION NUMBER: PCT/US98/12125
APPLICATION NUMBER: PCT/US98/12125
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RESULT 2
US-09-209-462B-150
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Best Local Similarity 99.7
Matches 318; Conservative
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LENGTH: 356 amino action
Type: (301) 309-8439
INFORMATION FOR SEQ ID NO: 145
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino action
Type:
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-06-13
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/209,462B CURRENT FILING DATE: 1998-12-11
                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                             OR APPLICATION NUMBER: 60/49,548
OR FILING DATE: 1997-06-13
OR FILING DATE: 1997-06-13
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/49,550
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/49,566
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/49,606
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/49,606
OR FILING DATE: 1997-06-13
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                                                                                     R APPLICATION NUMBER:
R FILING DATE: 1997-06
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                                        APPLICATION NUMBER: 60/
FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/
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               APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen et al.
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              NUMBER:
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Pred. No. 4.6e-207;
Pred. No. 4.6e-217;
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; TYPE: PRT
; ORGANISM: Homo sapiens
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Best Local Similarity
Matches 318; Conserv
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PRIOR FILING DATE: 1997-10-02
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R FILING DATE: 1997-09-12
OR APPLICATION NUMBER: 60/05
OR FILING DATE: 1997-09-12
OR APPLICATION NUMBER: 60/05
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OR APPLICATION NUMBER: 60/05
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OR FILING DATE: 1997-09-12
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PR FILING DATE: 1997-06

PR FILING DATE: 1997-06

PR FILING DATE: 1997-06

PR APPLICATION NUMBER:

PR FILING DATE: 1997-07

PR APPLICATION NUMBER:

PR FILING DATE: 1997-07

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FILING DATE: 1997-10-02
APPLICATION NUMBER: 60/0
FILING DATE: 1997-10-02
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FILING DATE: 1997-10-
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FILING DATE: 1997-09-12
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TPDSLSSGSSRDVQGTDAS
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                                                             QHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPG
                                                                                                                          SEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALT
                                                                                                                                                                        RASSGLPRNTVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINV
                                              QHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPG
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Pred. No. 4.6e-207;
0; Mismatches 1;
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Gaps

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206 146 146

266 266 206

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TPDSLSSGSSRDVQGTDAS

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PCT-US01-04098A-3196
PCT-US01-04098A-3196, Application PC/TUS0104098A
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-029
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                                                    PRIOR APPLICATION NUMBER: 09/728,422
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/663,561
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/654,936
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PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: CUSTOM
SEQ ID NO 2351
LENGTH: 378
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Best Local Similarity
Matches 318; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: PCT/US01/03800A
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: PCT/US01/04098A CURRENT FILING DATE: 2001-02-05
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APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: Not Yet Assigned PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: 09/620,325 FILING DATE: 2000-07-19
                                        FILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEGTRESAINVAEGKKQAQTLASEAEKAEQINQAAGEASAVLAKAKAKALAIRILAAALT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPDSLSSGSSRDVQGTDAS 345
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RESULT 5
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; ORGANISM: Homo sapiens PCT-US01-04942A-222
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Best Local Sim
Matches 318;
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                                                     SEQ ID NO 222
LENGTH: 3007
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 222,
                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: PCT/US01/04942A
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR ETLING DATE: 2000-09-19
PRIOR PLICATION NUMBER: 09/616,847
PRIOR APPLICATION NUMBER: 09/616,847
PRIOR FILING DATE: 2000-07-14
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PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
                                                                                                       PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/596,193 PRIOR FILING DATE: 2000-06-17
                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Novel Nucleic Acids and FILE REFERENCE: 21272-045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 3960
                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hyseq,
                                      TYPE: PRT
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Pred. No. 4.9e-207;
0; Mismatches 1;
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CURRENT APPLICATION NUMBER: PCT/USO1/08656
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 09/22,929
PRIOR ETLING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
SOFTWARE: Custom
SEQ ID NO 10594
LENGTH: 3019
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PCT-US01-08656-10594
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                                                                                      Query Match
Best Local S
Matches 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hyseq,
                                                                                                                                                     -US01-08656-10594
                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(3019)
OTHER INFORMATION: Xaa = X or * as
                                                                                                                                                                                                   NAME/KEY: DOMAIN
LOCATION: (2426)..(2903)
OTHER INFORMATION: identified by PFam, accession name AAA, E-value=3.3e-182, PFam
OTHER INFORMATION: score of 618.7
                                                                                                                                                                                                                                                                NAMEXKEY: DOMAIN
LOCATION: (115)..(144)
OTHER INFORMATION: Band 7 protein family proteins domain identified by eMATRIX,
OTHER INFORMATION: accession number BL01270C, p-value-6.745e-17, raw score of 16.91
                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALT 266
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                                    RASSGLPRNTVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINV 86
PEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKV 146
                                                                                       Conservative
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                                                                                       0;
                                                                                      Score 218; DB 1;
Pred. No. 3.8e-206;
0; Mismatches 1;
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                                                                                                               Length 3019;
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; ORGANISM: Homo sapiens 
'US-09-298-733-36
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CURRENT FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: 60/082,961
EARLIER FILING DATE: 1998-04-24
EARLIER APPLICATION NUMBER: 60/086,402
EARLIER FILING DATE: 1998-05-22
EARLIER APPLICATION NUMBER: 60/088,'994
EARLIER APPLICATION NUMBER: 60/089,163
EARLIER APPLICATION NUMBER: 60/089,163
EARLIER APPLICATION NUMBER: 60/089,163
EARLIER APPLICATION NUMBER: 60/089,163
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                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 36
LENGTH: 305
TYPE: PRT
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Best Local Similarity
Matches 202; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Secreted Prote TITLE OF INVENTION: Encoding Them FILE REFERENCE: AGI99-02pM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 60/091,619 EARLIER FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                             204 VLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAA 263
                                                                                                                                                                                                    144 DKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRAT 203
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VPGTPDSLSSGSSRDVQGTDAS
                                                                                                           VLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAA
                                                                                                                                                                                   DKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRAT 152
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ilarity 100.0%;
Conservative (
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 345
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; SOFTWARE: FastSEQ for W:
; SEQ ID NO 36
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-298-733A-36
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TITLE OF INVENTION: Secreted Proteins and Polynucleotides
TITLE OF INVENTION: Encoding Them
FILE REFERENCE: 1966 1009-000
CURRENT APPLICATION NUMBER: US/09/298,733A
CURRENT FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: 60/082,961
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/086,402
PRIOR APPLICATION NUMBER: 60/086,402
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/088,994
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                                                                                                                                                                                                               Sequence 36, Application US/09723594 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Raplejko, Peter
TITLE OF INVENTION: Secreted Proteins and Polynucleotides
TITLE OF INVENTION: Encoding Them
FILE REFERENCE: 1966.1009-002
CURRENT FALLATION NUMBER: US/09/723,594
CURRENT FILLING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/298,733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-07-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202;
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                                                                                                                                    Hoffmann, Heidi
Hall, Jeff
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Yuan, Olive
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SEQ ID NO 36
: LENGTH: 305
: TYPE: PRT
: ORGANISM: Homo sapiens
                                                                                                                                                                      APPLICANT: Rapiejko, Peter
TITLE OF INVENTION: Secreted Proteins and P
TITLE OF INVENTION: Secreted Proteins and P
TITLE OF INVENTION: Encoding Them
FILE REFERENCE: 1966.1009-001
CURRENT APPLICATION NUMBER: US/09/724,497
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/289,733
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-24
PRIOR APPLICATION NUMBER: 60/082,961
PRIOR APPLICATION NUMBER: 60/086,402
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/088,994
PRIOR APPLICATION NUMBER: 60/089,163
PRIOR APPLICATION NUMBER: 60/089,163
PRIOR APPLICATION NUMBER: 60/089,163
PRIOR APPLICATION NUMBER: 60/089,163
PRIOR APPLICATION NUMBER: 60/089,163
PRIOR APPLICATION NUMBER: 60/089,163
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SOFTWARE: Fas
SEQ ID NO 36
FRIGHT: 305
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Best Local Similarity
Matches 202; Conserv
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PRIOR APPLICATION NUMBER: 60//
PRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 79
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                                                                                                         NUMBER OF SEQ ID NOS
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                       LENGTH: 30
TYPE: PRT
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 VLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAA
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Yuan, Olive
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                                                                Query Match
Best Local
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Best Local Similarity
                                                    Matches
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                                                                                                                                                                                TELEFAX: (301) 309-8439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER RÉADABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: 86 Human Secreted Proteins NUMBER OF SEQUENCES: 318
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ADDRESSEE: Human
STREET: 9410 Key
CITY: Rockville
STATE: Maryland
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hes 202;
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                                                                                                                                                    LENGTH:
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                                                               Similarity
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9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                   Conservative
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100.0%; Pr
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                                               Score 202; DB 1; L
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                             60/060,841
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                                                           60/060,834
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Query Match

Length 358

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; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-04098A-1228
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-209-462B-411
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                                                                            NUMBER OF SEQ ID NOS: 3960
SOFTWARE: Custom
SEQ ID NO 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
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SEQ ID NO 411
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-029
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: Not Yet Assigned PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: 09/728,422 PRIOR FILING DATE: 2000-11-30 PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: PCT/US01/04098A CURRENT FILING DATE: 2001-02-05
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PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,060
PRIOR FILING DATE: 1997-10-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94
                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/620,325 FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                           FILING DATE: 2000-09-15
APPLICATION NUMBER: 09/654,936
FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/693,325 FILING DATE: 2000-10-20 APPLICATION NUMBER: 09/663,561
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APPLICATION NUMBER: 60/
FILING DATE: 1997-10-02
                                                                                                                                                                          APPLICATION NUMBER: 09/560,875 FILING DATE: 2000-04-27
                                                                                                                                                                                                              APPLICATION NUMBER: 09/598,075
FILING DATE: 2000-06-20
                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAP
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                                                                                                                                        DATE:
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UMBER: 60/061,059
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/04
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/04
PRIOR FILING DATE: 1997-06-13
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PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/
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                               PRIOR APPLICATION NUMBER: 60/058,668
                                                                  PRIOR APPLICATION NUMBER: 60/PRIOR FILING DATE: 1997-09-12
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PRIOR APPLICATION NUMBER:
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APPLICATION NUMBER: 60/058,669 FILING DATE: 1997-09-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVP
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99.7%;
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No. 3.3e-187;
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PRIOR APPLICATION NUMBER: 60/061
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 737
SOFTWARE: PALENTIN VET: 2.0
SEQ ID NO 416
LENGTH: 60
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-209-462B-416
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Best Local Similarity 100
Matches 58; Conservative
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CURRENT FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: PCT/US98/12125
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TITLE OF INVENTION:
FILE REFERENCE: PZ
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PRIOR FILING DATE: 1997-06-13
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PRIOR APPLICATION I
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OR FILING DATE: 1997-09-12
OR APPLICATION NUMBER: 60/06
OR FILING DATE: 1997-10-02
OR APPLICATION NUMBER: 60/06
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R APPLICATION NUMBER: 60/0
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BR FILLING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/04
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FILING DATE: 1997-06-13
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SOFTWARE: PatentIn V
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                                                       16.3%; Score 58; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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Search completed: September 22, 2002, 18:34:49 Job time: 252 sec

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1: /cgn2_6/ptodata/1

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US-08-293-284A-25
US-08-293-284A-32
US-08-293-008A-4
US-08-93-1025-3
US-08-677-304-3
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US-08-995-172-1
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US-08-891-322-6
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Sequence 2, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 5, Appli	Sequence 2, Appli	`	•	•	•	•	`	•	Sequence 1, Appli	Sequence 2, Appli

ALIGNMENTS

Sequence 1, Application US/08781562 Patent No. 5763589 GENERAL INFORMATION: ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-0 TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEPHONE: 415-845-4166 INFORMATION FOR SEQ ID NO: ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette SEQUENCE CHARACTERISTICS: LENGTH: 356 amino acids TYPE: amino acid IMMEDIATE SOURCE: LIBRARY: Consens CLONE: Consensus COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US FILING DATE: Herewith CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICANT: Hillman, Jennifer L. APPLICANT: GOIL, SUTYA K. TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS APPLICATION NUMBER: FILING DATE: TOPOLOGY: STRANDEDNESS: Consensus linear single US/08/781,562 PF-0181 US

99.4%; 100.0%;

Score 354; Pred No.

0; DB

Length 356;

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RESULT 2
US-08-346-849-25
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US-08-346-849-25
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Patent No. 5
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APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
                                                                                                       TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                          PRIOR APPLICATION NUMBER: 07/973,326
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: BTOOK, DAVID E:
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008
                                                                                                                                                                                                                                                                                                                  COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
COLOREST COMPANY DESCRIPTION DATA:
APPLICATION NUMBER: US/08/346,849
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APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
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CITY: Lexington
STATE: Massachu:
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                  TYPE:
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RESULT 4
US-08-293-284A-25
; Sequence 25, Application US/08293284A
; Patent No. 595343
; GENERAL INFORMATION:
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US-08-346-849-32
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Matches 7
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                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Holmes, Todd
TITLE OF INVENTION: SELFI
TITLE OF INVENTION: THERI
TITLE OF INVENTION: THERI
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
                                                                                                                   251 AKAKAEA 257
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1 AKAKAEA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK,
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lockshin, Curtis
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 AKAKAKA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Militia | CITY: Lexington STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 02173-4799
                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                        Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                        amino acid
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, 100.0%; Pr
                                                                                                                                                                                                        2.0%; Score 7;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STABLE MACROSCOPIC MEMBRANES FORMED BY SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7; DB 1; Pred. No. 5.8;
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                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                        Length 16;
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                     Patent No.
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APPLICATION NUMBER: 07/973,326

FILING DATE: 28-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: MIT-600

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                               APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: DiPersio, C. Michael
APPLICANT: Lockshin, Curtis
                               CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C STREET: Two Militia Drive
                                                                                                             TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                             APPLICANT:
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ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTITIES AND USES TITLE OF INVENTION: THEREFOR .
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                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                           249 AKAKAKA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 22-AUG-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Lexington
STATE: Massachus
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                     CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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5955343
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Massachusetts
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DiPersio, C. Michael
Lockshin, Curtis
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                                                                                           THEREFOR : 64
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Best Local Similarity
Matches 7; Conserv
               COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-POS

SOFTWARRE: PAtentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/993,008A

FILING DATE: 18-DEC-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/032,436

FILING DATE: 18-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: SULLIVAN, Sally A.

REGISTRATION NUMBER: 32,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08993008A Patent No. 6153596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,28
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APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Liotta, Dennis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 AKAKAEA 257
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                        STATE:
REFERENCE/DOCKET NUMBER:
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Pohl, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Petros, John A.
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Query Match
Best Local Similarity
Thes 7; Conserv
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                                                                                      TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Appli Patent No. 553461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US
APPLICATION NUMBER: PCT/US
FILING DATE: 14 - AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROHM, Benita J.
REGISTRATION NUMBER: 28,66
REFERENCE/DOCKET NUMBER: F
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MOLECULE TYPE: pe
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ORGANISM: N/A
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 908-276-3344
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 512 Spring
CITY: Cranford
STATE: New Jersey
                                                               STRANDEDNESS:
TOPOLOGY: N//
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/152,488 FILING DATE: 12-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                         TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stanley, James C.
VENTION: NOVEL PEPTIDES FOR HEPARIN AND
VENTION: LOW MOLECULAR WEIGHT HEPARIN
VENTION: ANTICOAGULATION REVERSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                              N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                               peptide
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                                                                                                                                                                                                                                                                                     PCT/US92/08069
                                                                                                                                                                                                                       28,664
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                                                                                                                                                                                                            RM-7WG
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Pred. No.
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; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-3
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                                                                                                                                                TELEFAX: 313-430 INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Applic Patent No. 5614494
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Best Local :
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                     FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MS-DOS v.6.22
SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy diskette 3.5"
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APPLICANT:
                                                                  PUBLICATION INFORMATION
                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                     TELEPHONE: 313-496-7622
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/303,025 FILING DATE: 08-SEPT-1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US92/06829 FILING DATE: 14-AUG-1992 APPLICATION NUMBER: US 08/152,488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Michig
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les 7; Conserv
                                                                                                                                                                                                                                                                                    NAME: Rohm, Benita J. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
DOCUMENT NUMBER: PCT/US92/08069 FILING DATE: 14-AUG-1993
                                                                                   ORGANISM:
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                                                  AUTHORS:
                                                                                                                                    TOPOLOGY:
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                                    N/A
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VENTION: NOVEL PEPTIDES FOR HEPARIN AND
VENTION: LOW MOLECULAR WEIGHT HEPARIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wakefield, Thomas W.
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                                                                                                                                N/A
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                                                                                                                  peptide
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Pred. No.
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Query Match

2.0%; Score 7;

DB 1;

Length

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PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-677-304-3
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                                    Query Match
Best Local Similarity luu.
Thes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             NAME: Rohm, Beniu. 28,664
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7
TELECOMMUNICATION INFORMATION:
mrt.EPHONE: 908-276-3344
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stanley, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS)Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             PUBLICATION INFORMATION:
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               249 AKAKAKA 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/152.488 FILING DATE: 12-NOV-1993 APPLICATION NUMBER: PCT/US92/08069
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CITY: Cranford
                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                            AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                           POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AKAKAKA 10
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                                                                                                                                                                                                                                                                                                                                      ENGTH:
4 AKAKAKA 10
                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Benita J, Rohm, Esq. 512 Springfield Avenue
                                                                                                                                                                                                                                                                                                                                      29 amino acids
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IVENTION: NOVEL PEPTIDES FOR HEPARIN AND IVENTION: LOW MOLECULAR WEIGHT HEPARIN
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No. 5721212 Relevant
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                                                          0; Mismatches
                                                                       Score 7;
Pred. No.
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
US-08-436-703B-8
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US-08-436-703B-8
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Matches
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                                                                                             Query Match
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APPLICANT: Wakefi
                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-965-1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WordPerfect (SOFTWARE: ASCII (DOS)TO CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: N/A FILING DATE: N/A ATTORNEY/AGENT INFORMATION: NAME: Rohm, Benita J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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                               249 AKAKAKA 255
                                                               Local Similarity hes 7; Conserv
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STREET: Suite 1525
                                                                                                                                                                                                                                                                     LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
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4 AKAKAKA 10
                                                                                                                                                                                                                                                       TOPOLOGY: N/A
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:: United States of America
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                                                               Conservative
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ASCII (DOS)Text
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08-MAY-1995
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100.0%; Fi
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                                                           %; Score 7; DB 2
%; Pred. No. 9.8
0; Mismatches
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                                                                            DB 2;
                                                                                         Length 29;
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US-08-995-172-18; Sequence 18, Application US/08995172B; Patent No. 6218112; GENERAL INFORMATION:

APPLICANT: Thatcher, David R

RESULT

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Best Local Similarity
Thes 7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-993-008A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/033,908 EARLIER FILING DATE: 1996-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/08/995,172B
CURRENT FILING DATE: 1997-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: OPt1 FILE REFERENCE: CACO0026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wilks, Paula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 35
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: UNSURE
LOCATION: (35)
OTHER INFORMATION: Xaa is Cys with Acm sidechain
                TELEFAX: 303-499-8089 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Polycationic Oligomers
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                       APPLICATION NUMBER: US 60 FILING DATE: 18-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 303-499-8080
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 AKAKAKA 255
                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 18-DEC CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 5370 |
CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                      REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 33
                                                                                                      REGISTRATION NUMBER:
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                                                 FELEPHONE:
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                                                                                                                     Sullivan, Sally
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Petros, John A.
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Pohl, Jan
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                                                                                                                                                                                                                         UMBER: US/08/993,008A
18-DEC-1997
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100.0%; Pr
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Pred. No.
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Query Match
Best Local Similarity
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                                                                                                                                                                                        TELEFAX: 303-49
INFORMATION FOR SEQ
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HYPOTHETICAL: 1
ANTI-SENSE: NO
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/993,008A FILING DATE: 18-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                  FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sullivan, Sally A.
                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Polycationic Oligomers
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                                                                                                 MOLECULE TYPE: PO
                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                       ANTI-SENSE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                      NAME: Sullivan, Sally REGISTRATION NUMBER:
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                                                                                                                                       TYPE: amino acid
STRANDEDNESS: no
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                                                                                                                                                                56 amino acids
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           Conservative
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249 AKAKAKA 255

В

2 AKAKAKA

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; LENGTH: 60 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-769-211-2
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; Sequence 2, Application US/08769211

; Patent No. 5830852

; Patent No. 5830852
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SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 6
                                    APPLICANT: Thatcher, David R
APPLICANT: Wilks, Paula E
TITLE OF INVENTION: Optimization of Gene Delivery and Gene Delivery Systems
FILE REFERENCE: CACCO0026
CURRENT APPLICATION NUMBER: US/08/995,172B
CURRENT FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: 60/033,908
EARLIER APPLICATION NUMBER: 60/033,908
EARLIER FILING DATE: 1996-12-23
NUMBER OF SEO ID NOS: 25
                                                                                                                                                                                                                                                            Sequence 6, Application US/08995172B Patent No. 6218112
                                                                                                                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 3255/02514
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9110
TELEFAX: 617-345-9111
FERMATION FOR SEO TO TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,211
FILING DATE: 18-Dec-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERfect 6.1
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thatcher et al.
TITLE OF INVENTION: Improved Pharmaceutical Compositions
TITLE OF INVENTION: Insulin-Receptor Mediated Gene Therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         249 AKAKAKA 255
                                                                                                                                                                                                                                                                                                                                                                                                  23 AKAKAKA 29
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STATE: Massa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kathleen M. Williams
REGISTRATION NUMBER: 34,38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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; OTHER INFORMATION: Description of Artificial Sequence: Peptide US-08-995-172-6
Вb
                    80
                                             Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                        LENGTH: 61
                       249 AKAKAKA 255
24 AKAKAKA 30
                                               Conservative
                                                           2.0%;
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                                                          Score 7; DB 4;
Pred. No. 19;
                                              Mismatches
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                                                                     Length 61;
                                               Indels
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                                             Gaps
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Search completed: September 22, 2002, 18:32:15 Job time: 343 sec

Copyright

GenCore version (c) 1993 - 2000

4.5 Compugen Ltd

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Result
No.
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Listing first 45 summaries
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length: 2000000000
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Match
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                     US-09-898-216-1
US-09-629-469A-11010
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US-60-389-987-768
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US-60-389-987-93-416
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(without alignments)
                                                                                                                                                                                                                                                                                                                                                   Sequence 1904, App
Sequence 768, App
Sequence 826, App
Sequence 39902, A
Sequence 5341, A
Sequence 51693, A
Sequence 61693, A
Sequence 61751, A
Sequence 140, App
Sequence 140, App
Sequence 75409, A
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98761, A
7, Appli
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416, App
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1904, Ap
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11010, A
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170.5	171.5	172.5	182.5	185	209.5	211	221	224	231	255.5	256.5	256.5	261	263.5	263.5	271	281.5	281.5
9.6	9.7	9.8	10.3	10.5	11.9	11.9	12.5	12.7	13.1	14.5	14.5	14.5	14.8	14.9	14.9	15.3	15.9	15.9
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Sequence 57280, A	Sequence 52568, A	Sequence 57141, A	Sequence 53682, A	Sequence 30739, A	Sequence 853, App	Sequence 422, App	-	Sequence 426, App	Sequence 415, App	-	Sequence 8455, Ap	Sequence 8455, Ap	Sequence 420, App	Sequence 3455, Ap	Sequence 3455, Ap	Sequence 4, Appli	•	Sequence 338, App

ALIGNMENTS

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LIBRARY: CONSENSUS
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SEQUENCE DESCRIPTION: SEQ
US-09-898-216-1
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; Sequence 1, Application US/09898216
; GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/781,562
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-018
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,216
FILING DATE: 02-ULI-2001
CLASSIFICATION: <Unknown>
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GOLI, SUTYA K.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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ADDRESSEE: Incyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3174 Porter Drive CITY: Palo Alto STATE; CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                     STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                            TYPE: amino acid
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                               ID NO:
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Query Match

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Score 1763;

DB 5;

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US-09-629-469A-11010
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PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 1999-300253
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
Best Local Matches 34
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APPLICANT: ISOG
APPLICANT: NISH
APPLICANT: HAYA
APPLICANT: SAIT
APPLICANT: YAMA
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                              Query Match
Best Local
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                                                                                                                      LENGTH: 356
TYPE: PRT
ORGANISM: Homo sapiens
-09-629-469A-11010
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OTSUKI, TETSUJI
TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING
FILE REFERENCE: 084335/0123
                                                                                                                                                                                                                                                     SOFTWARE: PatentIn
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nes 356; Conserva
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 2000-241899 FILING DATE: 2000-06-09 APPLICATION NUMBER: 60/159,590 FILING DATE: 1999-10-18
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     341;
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                         Similarity
                                                                                                                                                                                                                                                                              SEQ ID NOS: 19025
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SUGIYAMA, TOMOYASU
WAKAMATSU, AI
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     Conservative
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Score 1646; DB 5; Length 356; Pred. No. 1.9e-111; Indels
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APPLICANT: Rosen et
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                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/049,606
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/049,607
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/049,608
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/049,609
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/049,610
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/049,611
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/049,611
OR APPLICATION NUMBER: 60/050,901
OR APPLICATION NUMBER: 60/050,901
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/050,901
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/050,901
OR FILING DATE: 1997-06-13
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                                                                                                                    APPLICATION NUMBER: 60/051,919
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/055,984
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FILING DATE: 1997-06-13
                       APPLICATION
                                                 FILING DATE: 1997-09-1
                                                                        FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/
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                         NUMBER:
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60/058,668 60/058,665 60/052,989

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PRIOR APPLICATION NUMBER: 09/209,462
PRIOR FILING DATE: 1998-12-11
PRIOR PELICATION NUMBER: PCT/US98/1212
PRIOR PELICATION NUMBER: PCT/US98/1212
PRIOR APPLICATION NUMBER: 60/049,547
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,549
PRIOR APPLICATION NUMBER: 60/049,549
PRIOR APPLICATION NUMBER: 60/049,550
PRIOR APPLICATION NUMBER: 60/049,566
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,566
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,566
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,666
PRIOR APPLICATION NUMBER: 60/049,666
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APPLICATION NUMBER: 60 FILING DATE: 1997-09-1 APPLICATION NUMBER: 60 FILING DATE: 1997-09-1

NUMBER: 60/058,669: 1997-09-12

60/058,750

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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Faby, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: IDENTIFIED IN
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PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/060,865
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,059
PRIOR APPLICATION NUMBER: 60/061,069
PRIOR APPLICATION NUMBER: 60/061,060
                                                                                                                                                       Sequence 1904, Appli GENERAL INFORMATION:
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Best Local Similarity
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PRIOR PELICATION NUMBER: 60/058,972
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
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PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/060,834
PRIOR FILING DATE: 1997-10-02
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Pred. No. 1
 THERAPEUTIC INTERVENTION IN THE MITOCHONDRIAL PRO
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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Thang, Bing
APPLICANT: Ghosn, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION;
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROFILE REFERENCE: 660088.465P2
В
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US-60-389-987-768
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                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/60/389,987
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 768
LENGTH: 342
TYPE: PRT
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CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 1904
LENGTH: 356
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                                                                 Matches
                                                                               Query Match
Best Local Similarity
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TYPE: PRT
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              17 LSTGFWPRSGRASSGLPRNTVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYV 76
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                                                              Score 1613.5; DB Pred. No. 4e-109; 3; Mismatches
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Pred. No. 6e-111;
2; Mismatches 1
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                                                                                               DB 7;
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TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVEN
TITLE OF INVENTION: TDENTIFIED IN THE MITOCHONDRIAD
FILE REFERENCE: 660088 465P2
CURRENT APPLICATION NUMBER: US/60/389,987
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 826
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GENERAL INFORMATION:
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Best Local 9
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APPLICANT:
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APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford
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                                                                                                                     KEGWEKGLRAPVEAERRKRATVLESEGTRESAINVAEGKKOAQI
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332; Conserv
                                                     EASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNP
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Gibson, Bradford W.
Taylor, Steven W.
Glenn, Gary M.
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                                                                                      -VEAERRKRATVLESEGTRESAINVAEGKKQAQITASEAEKAEQINQAAG
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  DEELDRVKMS
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RESULT 7
US-10-219-793-411
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PRIOR APPLICATION NUMBER: 60/049,566
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OR APPLICATION UNMBER: 60/058,669
OR FILING DATE: 1997-09-12
OR APPLICATION NUMBER: 60/058,750
OR FILING DATE: 1997-09-12
OR FILING DATE: 1997-09-12
OR FILING DATE: 1997-09-12
OR FILING DATE: 1997-09-12
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DR APPLICATION NUMBER: 60/055,984
DR FILING DATE: 1997-08-18
DR APPLICATION NUMBER: 60/058,665
DR FILING DATE: 1997-09-12
DR APPLICATION NUMBER: 60/058,668
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FILING DATE: 1997-06-13
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APPLICATION NUMBER: 60/049,608
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APPLICATION NUMBER: 60/061,060 FILING DATE: 1997-10-02 R OF SEQ ID NOS: 737
                                                                             FILING DATE: 1997-10-02
APPLICATION NUMBER: 60/060,865
FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60/060,834
FILING DATE: 1997-10-02
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                                               APPLICATION NUMBER: FILING DATE: 1997-1
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APPLICATION NUMBER: 60/060,841
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APPLICATION NUMBER:
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SEQ ID NO 411

SOFTWARE: PatentIn

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; TYPE: PRT ·
; ORGANISM: Homo sapiens
US-10-219-793-411
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US-10-219-999-39902
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Best Local S
Matches 304
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PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 39902
LENGTH: 275
                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                   APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
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APPLICANT:
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                                          160 AINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAE 219
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nes 304; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASE 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASE 180
                                                                                                                                                                                                                                                                                                                                                                                                            Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                         Kovalic, David K.
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Hinkle, Gregory J.
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                                                                                                      35.1%; Score 619.5; DB 6;
48.2%; Pred. No. 4.1e-37;
tive 47; Mismatches 77;
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Pred. No. 1.9e-100;
Mismatches
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                                                                                                       Indels
                                                                                                                                    275;
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PRIOR APPLICATION NUMBER: US 60/312,544

PRIOR FILING DATE: 2001-09-21

NUMBER OF SEQ ID NOS: 63520

SEQ ID NO 55341

LENGTH: 283

TYPE: PRT
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US-10-219-999-55341
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                                Sequence 51693, Application US/10219999
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 55341, Application US/10219999 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
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APPLICANT: Stein, Joshua
TITLE OF INVENTION: cDNA SEQUENCES AND USES
FILE REFERENCE: 38-10(52726)C
                    APPLICANT:
                                                                                                                                                                                                                                                                       188 ESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASE 230
                                                                                                                                                                                                                                                                                                                                    192
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                                                                                                                                                                                                                                                         252 QAMEMQAEAERKKRAQILES-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 APALSRSFSRFNPRDDSSMFDPPEPPVNWGVSIVPEKKAYVVERFGKYLKTLGSGFHLLI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                  PVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKKTAQILESEGAMLDLANRAKGAAEAILAKSEATARGMRLVSDAMTTEGSAKAASLKLA 180
                                                                                                                                                                                                                                                                                                                                                                     QLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVK 187
                                                                                                                                                                                                                                                                                                                                  QLAQTTMRSELGKITLDKTFEERDALNEKIVSAINEAATDWGLKCIRYGIRDINPPAGIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AINEAATDWGLKCIRYEIRDINPPAGIRQAMEMQAEAERKKRAQILESEGMKQAQILESE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119;
INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
                    Stein,
                  Liu, Jingdong
Stein, Joshua
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53.4%;
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US-09-898-216-6
; Sequence 6, Application US/09898216
; GENERAL INFORMATION:
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Best Local Similarity
Matches 123; Conserv
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SEQ ID NO 51693
LENGTH: 263
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 SSRDVQGTDASXDEELDRVK 354
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                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,216
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: B1111ngs, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0181 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/781,562

FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPPLIEEADSNQTFSLQRPK 260
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                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CA
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                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 98751
LENGTH: 305
TYPE: PRT
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Best Local Similarity
Matches 110; Conserv
                                                                                Matches
                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 EPSPVEDQPKHAADGDDAEVAGWFSTDTDPS 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 RGVLDEATGRWGLRVARVELRSIDPPPSIQASMEKQMKADREKRAMILTAEGTREAAIKQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 TKAPVPGTPDSLSSGSSRDVQG----TDAS 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 QHNGDAAASLTVAEQYVSAFSKLAK-DSNTI-LLPSNPGDVTSMVAQAMGVYG-----AL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 AEGKKQAQ------ILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
38 VLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNV 97
                                                                                Local Similarity
les 98; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEGQKQAQILAAEGAKQAAILAAEADRQSRMLRAQGERAAAYLQAQGQAKAIEKTFAAI- 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLNIDTVVYFQVTVPQAAVYEISNYIVGVEQLTTTTLRNVVGGMTLEQTLTSRDQINAQL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --KAGRPTPEMLAYQYLQTLPEMARGDANKVWVVPSDFNAALQGFTRLLGKPGEDGVFRF 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: Owl
CLONE: 79701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 381 amino acids
                                                                                Conservative
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                                                                                                 26.4%;
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                                                                                76;
                                                                              Score 466; DB 5;
Pred. No. 6.5e-26;
6; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 123;
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                                                                                Indels
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RESULT 13
US-09-602-777A-140
; Sequence 140, Application US/09602777A
; GENERAL INFORMATION:
Markus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/141031 PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/602,777A CURRENT FILING DATE: 2000-06-23
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               OR ETLING DATE: 1999-07-14

OR APPLICATION NUMBER: DE 19932973.7

OR FILING DATE: 1999-07-17

OR APPLICATION NUMBER: DE 19933002.6

OR APPLICATION NUMBER: DE 19933003.4

OR APPLICATION NUMBER: DE 19933003.4

OR FILING DATE: 1999-07-14

OR APPLICATION NUMBER: DE 19933005.0

OR FILING DATE: 1999-07-14

OR APPLICATION NUMBER: DE 19933006.9

OR FILING DATE: 1999-07-14

OR APPLICATION NUMBER: DE 19933006.9

OR APPLICATION NUMBER: DE 19933006.9

OR APPLICATION NUMBER: DE 19933006.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932126.4
FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: DE 1932933.8 FILING DATE: 1999-07-14 APPLICATION NUMBER: DE 19932935.4
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: DE 19932924.9 FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: DE 19932922.2 FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: DE 19932920.6 FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: DE 19932129.9 FILING DATE: 1999-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932128.0
FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: DE 19932930.3 FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: DE 19932226.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: DE 19932127.2
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: DE 19932928.1
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Zelder, Oskar
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DATE:
1999-08-31
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                                                                                                                                                                              ; ORGANISM: Aquifex aeolicus US-09-791-537-75409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-791-537-75409
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PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941390.8
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941391.6
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19942088.2
PRIOR FILING DATE: 1999-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 140
LENGTH: 432
TYPE: PRT
                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 75409
LENGTH: 253
TYPE: PRT
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Best Local Similarity
Matches 112; Conserv
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                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 75409, Application US/09791537
                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bionomix, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 APV----PGTPDSLSSGSSRDVQGTDASXD 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 VDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINV
                    82 TVAIDIVVTFQINEPERAIYGVDNYIVGVEQISVATLRDVVGGMTLEETLTSRDVINRRL 141
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15 VLLFLASAIKVIPEYERAVVFRLGRVIGAKGPGLIIVIPIIDRIVRV-SLRTVTLDVPTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEGKKQAQILASEAEK------AEQ---INQAAGEASAVLAKAKAKAEAIRILAAALT 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QHNGDAAASLT - - - VAEQYVSAFSKLAKD - - SNTILLPSNPGDVTSMVAQAMGVYGALTK
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                                                                              Conservative
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                                                                          21.3%; Score 376.5; DB 5
39.3%; Pred. No. 1.6e-19;
Live 47; Mismatches 64
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Sequence 2, Application US/09458180

Sequence 2, Application:
APPLICANT: DIVERSA CORPORATION

APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Ronald V.
APPLICANT: Short, Jay M.

TITLE OF INVENTION: NUCLEOTIDE SEQUENCE OF THE AQUIFEX
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE OF THE ACUIFEX

CURRENT FILLS DATE: 1997-12-08
PRIOR APPLICATION NUMBER: US/09/458,180

CURRENT FILLNG DATE: 1999-12-08
PRIOR FILLNG DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 576775
TYPE: PATE
CORGANISM: Aquifex aeolicus
US-09-458-180-2
                                                                                                                                           á
                                                                                                                                                                                Db 553541 REKINMKLQEIIDROTDPWGVKVIAVELKKIDLPEELRKALARQAEAERERRAKIISAEA 553600
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                                                                                                    Db 553601 EYQAAQKLLEA---ARILAQE 553618
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US-09-458-180-2
Search completed: September 22, 2002, 18:30:32 Job time: 635 sec
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 21.3%; Score 376.5; DB 5; Length 576775; Best Local Similarity 39.3%; Pred. No. 4e-15; Matches 79; Conservative 47; Mismatches 64; Indels 11; Gaps
                                                                                                                            210 TRESAINVAEGKKQAQILASE 230 ::| : | |:||| |
                                                                                                                                                                                                              150 RESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 EYQAAQKLLEA---ARILAQE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 TRESAINVAEGKKQAQILASE 230 ::| : | |:||| |
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Title: Perfect score:

OM protein -

A97030
E97030
E770378
AC2354
C644035
C764403
D72522
C64403
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C669104
C71527
A835961
B95981
T34691
T34691

membrane membrane

protein protein erythrocyte band hypothetical prote conserved hypothet

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probable erythrocy stomatin-like prot probable erythrocy probable stomatin-probable stomatin-

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erythrocyte band

ALIGNMENTS

Scoring table:

Searched:

Minimum

Maximum

DB

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Database

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Post-processing: Minimum Match 0%
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2: pir2:*
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4: pir4:*
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Match
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1 MLARAARGHWGPFA
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Gapop 10.0 ,
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Listing first 45 summaries
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A;Introns: 2/3; 48/3; 82/1; 101/3; 135/3; 194/3; 243/1; 269/3; 312/3
C;Superfamily: erythrocyte band 7 integral membrane protein
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A; Residues: 1-357 < LAM>
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Best Local S
Matches 332
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                                                                                                                                                             KEGWEKGLRAPVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAG
                                                                                                                                                                            EASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNP
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118.4
118.3
118.3
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2

Score 1605; DB 2; Pred. No. 2.9e-98; 2; Mismatches 4

2:

Length 357; Indels

16;

Gaps

2

183 193 123 136

242

243

303

Result No.

Score

160.5 861.5 861.5 861.5 826 818.26 810.6 810.6 800.5 499.5 499.5 499.5 499.5 486.4 486.4 487.5 486.5 486.5 486.5 486.5 486.5 486.5 486.4 486.5 486.5 486.5 486.5 486.5

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R:Barlow, K.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19442
A;Accession: T21562
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 1
A;Introns: 16/2; 68/3; 124/3; 227/2
C;Superfamily: erythrocyte band 7 integral membrane protein
             A;Map position: 2
A;Introns: 72/2; 265/2
C;Superfamily: erythro
                                                                                       A; Experimental source: C; Genetics:
                                                                                                                            A; Molecule type: DNA
A; Residues: 1-354 <LYN>
A; Cross-references: EMB
                                                                                                                                                                                                    C:Accession: T39599
R:Lyne, M.: Wood, V.: Rajandream, M.A.: submitted to the EMBL Data Library, May A;Reference number: Z21866
A;Accession: T39599
                                                                                                                                                                                                                                                                                             conserved hypothetical protein SPBC16G5.07c - fission yeast (Schizosaccharomyces
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
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A; Residues: 1-334 <WIL>
A; Cross-references: EMBL: Z81072; PIDN: CAB03018.1;
                                                                   A; Gene: SPDB:SPBC16G5.07c
                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
Matches 188; Conserv
             Superfamily: erythrocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRSEVGKINLDTVFKERELLNENIVFAINKASAPWGIQCMRYEIRDMQMPSKIQEAMQMQ 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYK---ASYGVEDPEYAVTQLAQTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSGLP-----RNTVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QNLREIAIEIPEQGAITIDNVQLRLDGVLYLRVFDPYKACDASYGVDDPEFAVTQLAQTT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSTLPLAVTSSRQAHAAHNTVINEVPQQEAWVVERMGKFYKILEPGLNFLLPIIDKIKFV 83
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                                                                                                                              EMBL: AL023554;
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               band 7 integral membrane protein
                                                                                                          972h-;
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                                                                                                                                                                                                                                           Barrell, B.G.;
1998
                                                                                                          c16G5
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                                                                                                                              GSPDB:GN00067;
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A; Molecule type: DNA
A; Residues: 1-515 <BEV>
A; Cross-references: EMBL: AL035602
A; Experimental source: cultivar C:
C; Genetics:
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A; Note: T29A15.70
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Best Local Similarity
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                                          ILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGAL 319
                                                                                                                                    KITLDKTFEERDTLNEKIVEAINVAAKDWGLQCLRYEIRDIMPPHGVRAAMEMQAEAERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSLYIAQQYIINFGKLAKASNSMIVPASTSDVSGMVAQALSIFKQVSKTTAPDKSTPKEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLN
                                                                                                                                                                                                                                                                  SSGLPRNTVVL-----FVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INVAEGDKQAEILDSEGQKIKTINSALAEAQAIREKASATASGIAVLADSIKKQEHGLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IHITDAINKAAESWGIRCLRHEIRDIRPPESVVMAMHQQVSAERQKRAEILESEGKRQAA
                                                                                            KRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIR 259
                                                                                                                                                           KLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERR 199
                                                                                                                                                                                        KEEAIPIPNQTAITKDNVSIHIDGVLYVKIVDPKLASYGVESPIYAVVQLAQTTMRSELG
                                                                                                                                                                                                               KEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELG 139
                                                                                                                                                                                                                                           SAGYPSNSFQLTPPTNWGIRIVPERKAFVIERFGKYATTLPSGIHFLIPFVDRIAYVHSL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170;
    TKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVK
                           LLSQSLKETGGVEAASLRVAEQYITAFGNIAKEGTIMLLPSGASNPASMIAQALTMYKSL
                                                                                 KRAQILESEGERQSHINIADGKKSSVILASEAAKMDQVNRAQGEAEAILARAQATAKGLV
                                                                                                                                                                                                                                                                                               168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                           133/3; 183/3; 203/1; 234/1; 267/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.8%;
56:7%;
                                                                                                                                                                                                                                                                                                          46.7%;
50.1%;
                                                                                                                                                                                                                                                                                              67;
                                                                                                                                                                                                                                                                                                                                                                                                                 Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 861.5; DB Pred. No. 2.1e-49
                                                                                                                                                                                                                                                                                                          Score 826;
Pred. No. 7.
                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 BAC
                                                                                                                                                                                                                                                                                                            DB 2;
.5e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                 clone
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                                                                                                                                                                                                                                                                                               ; 08
                                                                                                                                                                                                                                                                                                                                                                            297/3;
                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                            317/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354;
                                                                                                                                                                                                                                                                                               20;
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                                                                                                                                                                                                                                                                                                                                                                            394/1; 451/3
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
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                                                                                                                                                                                                                                                                                               2
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ດ : :

-VINGPSKDHQETQALDETDLEELE

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hypothetical protein RC0452 [imported] - Rickettsia conorii (strain Malish C;Species: Rickettsia conorii C;pacies: Rickettsia conorii C;ate: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001 C;Accession: D97756 R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; S; Science 293, 2093-2098, 2001 Science 293, 2093-2098, 2001 A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowa: A;Reference number: A97700; MUID:21442074; PMID:11557893 A;Accession: D97756
                                                                                                                                                                                                                                                                                                                                    hypothetical protein RP328 - Rickettsia prowazekii C:Species: Rickettsia prowazekii C:Species: Rickettsia prowazekii C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 C:Accession: B71689 C:Accession: B71689 R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T. Nature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
B71689
                                                                                                                                     A; Gene: RP328 C; Superfamily: erythrocyte band 7 integral membrane
                                                                                                                                                                                           A;Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14788.1; PID:g386080
A;Experimental source: strain Madrid E
                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-311 <AND>
                                                                                                                                                                                                                                                                                 A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria A;Reference number: A71630; MUID:99039499
A;Accession: B71689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE006914; PIDN:AAL02990.1; PID:g15619524; GSPDB:GN00173 C;Genetics:
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                                                                                                                                                                              C; Genetics:
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                                                                                                                                                                                                                                                             A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                   Query Match
Best Local S
Matches 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259
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                    37
                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVAAINQAAINWGIQCMRYEIKDIQPPQTILKAMELQVAAERQKRAQILESEGNRQAKIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNAS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
Conservative
                                                     Conservative
                                                                   45.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.9%;
                                                     60;
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                                                   Score 806; DB 2;
Pred. No. 7.9e-46;
0; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 811.5;
Pred. No. 3.
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                                                     69;
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                                                                                                                                         protein
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                                                                                    Length 311;
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                                                   Indels
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                    96
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                                                                                                                                                                                                                                                                                                                                                   T.;
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                                                   0;
                                                                                                                                                                                                                                                                                                                                                      Alsmark,
                                                              probable periplasmic protein NMA1382 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: H81907
            R;Parkhill, J.; Achtman, M.; ; Holroyd, S.; Jagels, K.; Lo
Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                              Ωy
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A;Title:
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Complete

DNA sequence of a

serogroup A strain of Neisseria menigitidis

M.; James, .; Leather,

K.D.; Bentley,
S.; Moule, S.;

S.D.; Churcher, C.; Klee, Mungall, K.; Quail, M.A.;

S.R.; Mo Rajandre

Z249

Z2491

8

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-374 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Lawson, D.; Bowman, S.; Barrell, I submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C0800w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun C;Accession: T18493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
T18493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position:
A; Note: C0800w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: Z18935
A; Accession: T18493
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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    291
                                       261
                                                                              242
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                                                                                                                                                                                                                                                                                                                                        FWPRSGRASSGLPRNTVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLK
                                                                                                 RATVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRI
                                                                                                                                                                             LSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGAL
ISNKIKKLDSNNAISLLVAEQYIDVFSNICKNNNTVIIPADLNNISSLISQSLSIY
                                       LAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVY 316
                                                                              RAEILQSEGERESEINIAIGKKRKSILIAE------
                                                                                                                                                        LTLDATFLERDNLNEKLYKAINESAKNWGIKCMRYEIRDIILPVNIKNAMEKQAEAERRK
                                                                                                                                                                                                                                       EETITIPNQTAITKDNVTLNIDGVLYIKCDNPYNSSYAIEDAVFAVTQLAQVTMRSELGK
                                                                                                                                                                                                                                                                            EIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGK 140
                                                                                                                                                                                                                                                                                                                      FWNHLG-----FVIIPQETAYIVERLGKYNKTLLAGIHFLIPFIDKIAYVFSLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAEGEKAQIVLNSEASYTDQVNRAKGEAEAIGLVATATANSIEIVAAAIQKTGGSDAVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAEAIRILAAALTQHNGDAAASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVSAINQAAINWGIQCMRYEIKDIQPPQTILKAMELQVAAERQKRAQILESEGNRQAKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTLSIDGVLYVKIIDPMAASYGVNNPYYAITQLAQTTMRSEIGKLPLDRTFEERDTLNVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVKVVPQQQAWVVEKLGKFDKVLQPGLNLLIPIIQRVAYKHTLKEEAIDVTAQTAISNDN
                                                                                                                                                                                                                                                                                                                                                                                                  138;
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: 298551;
                                                                                                                                                                                                                                                                                                                                                                                                                   40.9%; Score 722; DB 2;
46.6%; Pred. No. 3.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                68;
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                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  68;
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  346
                                                                                                                                                                                                                                                                                                                                                                                              Caps
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A;Authors: Grandl, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stomatin/Mec-2 family protein NMB1220 [imported] - Neisseria meningitidis (strain c;Speckes: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: F81107
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A:Experimental source: serogroup
C:Genetics:
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A; Accession: H81907
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-315 < PAR>
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C; Superfamily:
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A; Residues: 1-315 <TET>
A; Cross-references: GB: AE002470;
A; Experimental source: serogroup
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C; Superfamily: erythrocyte
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                                                                                                                                          VPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQ 100
                                         IDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESE- 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRE 149
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                       VDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVAA
                                                                                                      IPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSLKEIPLDVPSQVCITRDNTQLT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAI 258
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B, strain MC58
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A, strain Z2491
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Pred. No. 6.6e-40;
                                                                                                                                                                                                  Score 712.5; DB : Pred. No. 1.1e-39
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                                                                           C;Accession: D75311
C;Accession: D75311
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E
M.; Shen, M.; Vamathevan, J.J.; Lam, P. S.; Smith, H.O.; Venter, J.C.; Fraser, C. Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresi A; Reference number: A75250; MUID:20036896
                                                                                                                                        conserved hypothetical protein - Deinococcus radiodurans (strain
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change
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the radioresistant bacterium MUID:20036896

Deinococcus

radiodurans

#text_change 17-Mar-2000

R1)

E.K.; Peterson, J.D.; , L.; Utterback, T.; Za

Zalewski,

Dodson,

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C;Species: Synechocystis sp.
A; Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 |
C;Accession: S74505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-321 <KAN>
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A; Accession: S74505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAEAIRQIAAALQTQG
QFLLAQQYLNMGTTIGSSDSSKVMFLDPRNILSTLEGVRSIVG
                                                                         SLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYG
                                                                                                                                              NSAQGDAQARVLEAEAKKKAAILNAEAEQQKKVLEAKATAEALSILTEKLSSDNHAREAL
                                                                                                                                                                                                                    NVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHN-GDAAA 274
                                                                                                                                                                                                                                                                                                 LLLRELDISTOPWGVKVTRVELRDIMPSKAVLDSMELQMTAERKKRAAILTSEGQRDSAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNA 155
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A; Accession: D75311
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-344 <WHI>
A; Cross-references: GB: AE002048; GI
A; Experimental source: strain R1
C; Genetics:
                                                                                                                                               A. Cross-references: GB:AE003872; GB:AE003849; NID:g9104975; FIDN:AAF82998.1; GSPDB:GN000.
A; Experimental source: strain 9a5c

R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; I Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, I Briones, M.R.S.; Bueno, M.R.P.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, I A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasal A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, A.C.; A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Vettore, A.L.; A.S.; Naces and A.S.; Nac
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A;Reference number: A82515; MUID:20365717 A;Note: for a complete list of authors see reference number A:59328 below
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C; Superfamily: erythrocyte
                                                                                                                              M.; Tsuhako, M.H.; Vallada, H.; A; Reference number: A59328
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A; Residues: 1-337 <SIM>
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Best Local s
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108; Conservative
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67; Mismatches
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n. J.; Ermolaeva, M.; White, O.; Salzberg; S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87667
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A; Residues: 1-310 <STO>
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: E87667
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                                            SLTVAEQYVSAFSKLAK--DSNTILLPSNPGDVTSMVAQAMGVYGALTK----
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Pred. No. 8.5e-25;
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conserved hypothetical protein YPO3083 [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB0375
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; II, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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A;Residues: 1-322 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74171.1; PID:g17131564; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: AIZ114
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ang A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AIZ114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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      A;Cross-references: GB:AL590842; PIDN:CAC92325.1; PID:g15981036; GSPDB:GN00175 C;Genetics:
                                                               A; Molecule type: DNA
A; Residues: 1-304 < KUR>
                                                                                                                                                     A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AB0375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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C;Superfamily: erythrocyte band 7 integral membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein alr2472 [imported] - Anabaena sp. (strain PCC 7120)
C;Species: Anabaena sp.
                                                                                                                           A; Status: preliminary
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Genetics:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 SNGTAEQALEVLLALGYLDMGATIGKSDSSKVMFMDPRAIPATLEGIRSIVSDS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 LRELDIATDPWGVKVTRVELRDIIPSQAVRESMELQMSAERRRRAAILNSEGEREAAVNS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 Match 27.3%; Score 482.5; DB 2; Local Similarity 37.1%; Pred. No. 1.5e-24; nes 109; Conservative 67; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIEVDAVVYWRIVDMEKAWYKVENLHSAMVNMVLTQIRSEMGQLELDQTFTARSQINELL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKVINQGNEVLVERLGSYHKKLGPGLNLVLPFIDKAVYKETIREKVLDIPPQKCITRDNV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NYFVAQKYVEAFAELARSPQQKTVIVPADFAGLTGTVA---GV-GELIKSLGADAPRPTP 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HNGDAAASLTV--AEQYVSAFSKLAK-DSNTIL-----LPSNPGDVTSMVAQA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARGKAEAQILDAEARQKSVILQAEAEQKAIVLKAQAERQQQVLKAQAIAESAEILAQKIS
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Best Local Similarity 34.3%;
Matches 99; Conservative 7:
                                     275 SLTVAEQYVSAFSKL--AKDSNTILLPSNPGDVTSMVAQAMGVYGALTK 321
                                                                                                                             216
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252 NYFVAQKYTDALQHIGSANNSKVIMMPLE-----ASSLMGAIGGIAE
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                                                                                                                                                                                                                                                                                                                                                                                       36 TVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLD 95
                                                                                                                        NVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAEAIRILAAALTQHNGD-AAA 274
                                                                                                                                                                                                SIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAI 215
                                                                                    LRAEGEKQSQILKAEGERQSAFLQAEARERA----AEAEAQATKMVSEAIAA--GDIQAI 251
                                                                                                                                                                                                                                                          NANVAIDAVCFIQVIDPVKAAYEVSNLELAIVNLTMTNFRTVLGSMELDEMLSQRDNINS 137
                                                                                                                                                                                                                                                                                  NVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                 72;
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Pred. No. 3.2e-24;
2; Mismatches 102;
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Search completed: September 22, 2002, 18:22:45 Job time: 3402 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
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16-OCT-2001 (Rel. 40, Last annotation
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
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Riley M., Collado-Vides J., Glasner J.D.,
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Hypothetical protein ybbK.
YBBK OR B0489 OR 20642 OR ECS0552.
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Hypothetical protein; Transmembrane; Complete proteome TRANSMEM 3 23
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InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
SMART; SM00244; PHB; 1.
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MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M.,
Methanobacterium thermoautotrophicum
                                  Hypothetical MTH692.
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                                                                                                                                                                                                                                                                                                                                                                    YFVAQKYTEALQQIGSSSNSKVVMMPL---EASSLMGSIAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDAINQAADCWGIRCLRYEIKDIHYPPRVKESMQMQVEAERRKRATVLESEGTRESAINV 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEGKKQAQILASEAEKAEQINQA-AGEASAVLAKAKAKAEAIRILAAALTQHNGD-AAAS 275
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Pred. No. 2.2e-23;
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   Hypothetical AF1420.
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Hypothetical protein; Transmembrane; Complete proteome TRANSMEM 2 22
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Pfam; PF01145; Band_7; 1.
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35425 MW;
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-i- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
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Hypothetical protein; Transmembrane; Complete proteome.

TRANSMEM 3 23 POTENTIAL.

SEQUENCE 249 AA; 28346 MW; 4AF8EAD58AF6F230 CRC64;
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Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
Archaeoglobus.
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                                                                                                                                           EYQAAMKLREA---ADVLA-QSEGAILLRYLQTLNEISAEQNTTI
                                                                                                                                                                        TRESAINVAEGKKQAQILASEAEKA-----EQINQAAGEASAVL 248
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                                                                                                                                                                                                                                                                                                                                                                                            Score 362; DB 1;
Pred. No. 8.5e-17
0; Mismatches 7
                                                                PRT;
                                                                199
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 249
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Loftus B.,
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Query Match
Best Local S
Matches 67
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MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Eleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodowsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus Sandaschi.";
                                                                                                YF11_PYRHO
059180;
30-MAY-2000
30-MAY-2000
16-OCT-2001
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                                                                  Hypothetical PH1511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
SMART; SM00244; PHB; 1.
SMART; SM00244; PHB; 1.
Archaea; Euryarchaeota; NCBI_TaxID=53953; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein;
TRANSMEM 7 2:
SEQUENCE 199 AA; 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                               Pyrococcus horikoshii
                                                                                                                                                                                       PYRHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U67526; AAB98826.1;
TIGR; MJ0827; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                         84
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                                                                                                                                                                                                                                                                                                                         VVKVDAVVYYRVIDVEKAILEVEDYEYAIINLAQTTLRAIIGSMELDEVLNKREYINSKL
                                                                                                                                                                                                                                                                                        VDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTR 211
                                                                                                                                                                                                                                                                                                                                         TLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASI 157
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                                                                                                  (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                  protein
                                                                                                                                                                      STANDARD;
                                                             39, Created)
39, Last sequence update)
40, Last annotation update)
ein PH1511.
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22809 MW;
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                                   Thermococcales; Thermococcaceae;
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Pred. No. 2e-16;
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2545CE07DD54337E CRC64;
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                                                                                                                                                                      266
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                                 Pyrococcus
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Best Local Similarity
Matches 72; Conserv
                                                                                                                                                                       16-OCT-2001
16-OCT-2001
16-OCT-2001
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"Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01270; BAND_7; 1.
Hypothetical protein; Transmembrane;
TRANSMEM 7 27 POTENTIA
SEQUENCE 266 AA; 2999 MW; 21D06F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
 structure
                                             STRAIN-ORSAY;
                                                            SEQUENCE FROM
                                                                                       Pyrococcus abyssi.
Archaea; Euryarchaeota;
NCBI_TaxID=29292;
                                                                                                                                         Hypothetical PAB1933.
                                                                                                                                                                                                                     YJ33_PYRAB
Q9V0Y1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
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                             Heilig R.;
             "Pyrococcus abyssi
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                                                                                                                                                                                                                                                                                                                                                                               142
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SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                               NVAEGKKQAQI-----LASEAEKAEQINQAAGEASAVL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNA 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NVPVRVNAVVYFRVVDPVKAVTQVKNYIMATSQISQTTLRSVIGQAHLDELLSERDKLNM 141
and
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(Rel. 40,
(Rel. 40,
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ilarity 33.0%;
Conservative 5
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. A
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   . genome
                                                                                                                                                       , Last sequence update) , Last annotation update) PAB1933.
                                                                                                                                                                                                      Created)
             sequence: insights
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Pred. No. 1.5e-14;
55; Mismatches 82
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; 21D06F199C31021F CRC64;
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                                                                                                         Thermococcaceae;
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              into
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              archaeal chromosome
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RESULT 9
BAN7_HUMAN STANDARD; PRT; 287 Am.
ID BAN7_HUMAN STANDARD; PRT; 287 Am.
AC P27105; Q14087; Q15609;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-CCT-2001 (Rel. 40, Last annotation update)
DT 16-CT-2001 (Rel. 40, Integral membrane protein (Stomatin) (Protein
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SMART; SM00244; PHB; 1.
PROSITE; PS01270; BAND_7; 1.
Hypothetical protein; Transmembrane; Complete
TRANSMEM 1 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                "The
band
                                                  SEQUENCE FROM N.A.
MEDLINE=96423038; PubMed=8825639;
Unfried I., Entler B., Prohaska R.
                                                                                                                                                                        Stratowa
                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
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                                                                                                                      Biochim.
                                                                                                                                        band
                                                                                                                                                                                      Hiebl-Dirschmied C.M., Entler B., Glotzmann
                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE=91355220; PubMed=1883838;
                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                      Stratowa C., Prohaska R.;
"Cloning and nucleotide sequence of cDNA band 7 integral membrane protein.";
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            ied I., Entler B., Prohaska R.;
organization of the gene (EPB72) encoding the
7 integral membrane protein (protein 7.2b).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AERRKRATVLESEGTRESAINVAEGKKQAQI-----LASEAEKAEQINQAAGEASAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPTNFFVTTIILLFILIFLASAIKIVKEYERAVIFRLGRVVGARGPGLFFIIPIFEK-AV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AERERRARITLAEAERQAAEKLREA---AEIISEHPMALQLRTLQTISDVASDKSNVI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVIGQAHLDELLSERDKLNMQLQRIIDEATDPWGIKVTAVEIKDVELPAGMQRAMAKQAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVDLRTQVLDVPVQETITKDNVPVRVNAVVY,FRVVDPVKAVTQVKNYIMATSQISQTTLR 121
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76; Conserv
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268 AA; 30241 MW; AE1FBBEBD48A4F84 CRC64;
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Pred. No. 3.8e-14;
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                                                                                                                                                      encoding human erythrocyte
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                                   human erythrocyte
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[3] SEQUENCE FROM N.A.

marrow;

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EMBL; X60067; CAA42671.1; -.
EMBL; X85116; CAA55436.1; -.
EMBL; X85117; CAA55436.1; JOINED.
EMBL; W81635; AAC50296.1; ALT_SEQ.
EMBL; U33931; AAC50296.1; JOINED.
EMBL; U33925; AAC50296.1; JOINED.
EMBL; U33927; AAC50296.1; JOINED.
EMBL; U33928; AAC50296.1; JOINED.
EMBL; U33928; AAC50296.1; JOINED.
EMBL; U33928; AAC50296.1; JOINED.
EMBL; U33928; AAC50296.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure, organization, and expression of the a candidate gene for hereditary hydrocytosis."; Biol. Chem. 270:26358-26363(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stewart G.W., Hepwort Argent A.C., Casimir Submitted (DEC-1991)
                                       DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Snyers L., Umlauf E., Prohaska R.;

*Cysteine 29 is the major painitoyiation site on stomatin.

*FEBS Lett. 449:101-104(1999).

-1- FUNCTION: THOUGHT TO REGULATE CATION CONDUCTANCE.

-1- SUBCELLULAR LOCATION: EXPOSED ON THE CYTOPLASMIC SURFA
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 4-24, AND PHOSPHORYLATION SITE MEDLINE=93385136; PubMed=8373790;
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                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                            PROSITE;
                                                                                                                                         PRINTS; PR00721; STO
SMART; SM00244; PHB;
                                                                                                                                                      InterPro; IPR001972; Stomatin.
pfam; pF01145; Band_7; 1.
pRINTS; PR00721; STOMATIN.
                                                                                                                                                                                  InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomati
                                                                                                                                                                                                             MIM; 185000;
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                                                                                   TRANSMEM
                             LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ialzer U., Ahorn H., Prohaska R.;
Identification of the phosphorylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       integral membrane protein: implications tructure.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content ified and this statement is not removed. Usage by an
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DISEASE: DEFECTS IN EPB72 IN RED CELLS OF PATIENTS WITH HEREDITARY
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                                                                                                                            PS01270; BAND_7; 1.
                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepworth-Jones B.J., Keen J.N., Dash B.J.C., Casimir C.M.; Casimir C.M.; C-1991) to the EMBL/GenBank/DDBJ databases.
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                          PALMITATE (PARTIAL).
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CYTOPLASMIC
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4B52FB2866ECC337 CRC64;
                                                                    (POTENTIAL)
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SEQUENCE
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Latreille P., Gattung S.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
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SMART; SM00244; PHB; 1.
PROSITE; PS01270; BAND_7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (SC or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                    Transmembrane; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01145; Band_7;
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomati
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LQIDGYLYLRIMDPYKASYGYEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIV 158 : : | | : | | | : | : | | : : | | | : : | | | : | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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7B55DF6C02268480 CRC64;
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                               EMBL; U50997; AAB18857.1; JOIN EMBL; U50998; AAB18857.1; JOIN MCD; MGI:95403; Epb7.2. InterPro; IPR001107; Band_7. InterPro; IPR001972; Stomatin.
                                                                                                                                                                                                                                                                                                                                                    "Genomic organization and 5'-flanking DNA stomatin gene (Epb72) ";
Genomics 34:410-412(1996).
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01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update
Erythrocyte band 7 integral membrane protein
7.28).
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01-OCT-1996 (Rel. 34, C
01-OCT-1996 (Rel. 34, L
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entities requires a
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Mammalia; Eutheria;
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          PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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L; U17297; AAA75024.1; -...
L; U50999; AAB18857.1; JOINED.
JL; U50994; AAB18857.1; JOINED.
JL; U50995; AAB18857.1; JOINED.
JL; U50995; AAB18857.1; JOINED.
JL; U50995; AAB18857.1; JOINED.
JL; U50996; AAB18857.1; JOINED.
JL; U50996; AAB18857.1; JOINED.
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(SEP-1995) to
                        Band_7;
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Rodentia;
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                                    Stomatin.
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thi; Muridae;
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Best Local S
Matches 63
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Q19958;
Q1-NOV-1997
01-NOV-1997
15-DEC-1998
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                                                    WormPep; F32A6.5; CE04473.
InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin
                                                                                                                                                                                                    Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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Caenorhabditis elegans.
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STO-2 OR F32A6
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30.7%;
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PALMITATE (PARTIAL) (BY SIMILARITY).

V -> A (IN REF. 2).

I -> F (IN REF. 2).

L -> I (IN REF. 2).

F -> L (IN REF. 2).

V -> I (IN REF. 1).

N -> H (IN REF. 1).
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Pred. No. 2.8e-11;
0; Mismatches 79;
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CYTOPLASMIC (POTENTIAL)
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PRINTS; PR00721; STOR SMART; SM00244; PHB;

STOMATIN.

Pfam; PF01145; Band_7;

Transmembrane;

Multigene family.

PROSITE;

PS01270;

BAND_7;

131

71 94

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STOL_CABELL
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InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
PRINTS; PR00721; STOWATIN.
SMART; SM00244; PHB; 1.
PROSITE; PS01270; BAND_7; 1.
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01-NOV-1997
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; SEQUENCE 281
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
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15-DEC-1998
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les 73; Conservative 6
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OR F08C6.4
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(Rel.
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                                                                                                               Multigene family. AA; 30481 MW; A
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31000 MW;
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                                   15.2%;
25.2%;
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Pred. NO. 7.2e-11;
4; Mismatches 78
              Score 269; DB 1;
Pred. No. 9.7e-11;
2; Mismatches 99
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                EMBL; U26736; AAA87552.1; -. EMBL; U26735; AAA87551.1; -. EMBL; U41021; AAA82333.1; -. EMBL; F14D12.4; CE04393.
InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
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Q27433;
Q1-NOV-1997 (Rel. :
01-NOV-1997 (Rel. :
01-NOV-1997 (Rel. :
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                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: POSITIVELY REGULATES THE ACTIVITY OF THE PUTATIVE MECHANOSENSORY TRANSDUCTION CHANNEL. MAY LINK THE MECHANOSENSORY CHANNEL AND THE MICROTUBULE CYTOSKELETON OF THE TOUCH RECEPTOR NEURONS. REQUIRED FOR THE FUNCTION OF A SET OF SIX TOUCH RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
MEDLINE-96069765; PubMed-7477350;
Huang M., Gu G., Ferguson E.L., Chalfie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                      between the Swiss Institute of Bioinfo
the European Bioinformatics Institute
                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                               NEURONS
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Best Local Similarity
                                                     WormPep; T04F8.5; CEL8926.
InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
SMART; SM00244; PHB; 1.
PROSITE; PS01270; BAND_7; 1.
                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
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SMART; SM00244; PHB; 1.
PROSITE; PS01270; BAND_7; 1.
                   Transmembrane; Multigene family. NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
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SEQUENCE 481 AA; 51899 MW;
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 213 AA;
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 23380 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.8%; Score 262; DB 1; 25.3%; Pred. No. 5.3e-10;
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; 37D2894AD39E040A CRC64;
D4EB210BB9D56B28 CRC64;
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DA---ADVIAT 196
                                                                                DAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVA 218
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                            EGKKQAQILAS 229
                                                       AALDEATDPWGVKVERVEIKDVRLPIQLQRAMAAEAEAARAAGAKIIAAEGEQLASRALA 188
                                                                                                                VSVDAVIYERISNATVSVINVEDAARSTKLLAQTTLRNFLGTRTLAEMLSSRDAISMQMQ 128
                                                                                                                             LQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIV 158
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28.8%;
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Search completed: September 22, 2002, 18:30:47 Job time: 545 sec

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Scoring table:
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2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_manmal:*
7: sp_mhc:*
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9: sp_phage:*
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Q9DCG8
Q9W1F7
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Q9dcq8 mus musculu
Q9dcq8 mus musculu
Q9w1f7 drosophila
Q9xvp9 caenorhabdi
O6(121 schizosacch
Q93vp9 arabidopsis
Q5t082 arabidopsis
Q51vw0 arabidopsis
Q51vw0 arabidopsis
Q51vw0 arabidopsis
Q52dk0 rickettsia
Q52dk0 rickettsia
Q52dk0 rickettsia
Q52dk0 rickettsia
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Q96fy2 homo sapien
Q9p042 homo sapien
Q60376 homo sapien
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RESULT Q9UJZ1

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067057	Q98RE1	Q9HSA8	OXZW6D	Q98H59	Q9RQU5	Q97K67	Q9CBM5	Q92M51	Q9UYE4	058205	Q9K458	Q9KTC6	Q9CME1	Q9F507	Q9x9Z6	Q9AHZ8	Q9A331	Q9PGW3	Q9RSI1	Q9U4M5	Q9JPN2	Q9JРН3	Q9K2T7	Q9JRD6	Q9JPG5	Q9JPN3	Q9JPH5	Q9JR80
~	_		_	Q98h59 rhizobium l	C	Q97k67 clostridium	Q9cbm5 mycobacteri	Q92m51 rhizobium m		058205 pyrococcus	Q9k458 streptomyce	Q9ktc6 vibrio chol	Q9cmel pasteurella		Q9x9z6 streptomyce	Q9ahz8 photorhabdu	_	Q9pgw3 xylella fas	_	Q9u4m5 leishmania	Q9jpn2 neisseria m	Q9jph3 neisseria m	=	99		Q9jpn3 neisseria m	Q9jph5 neisseria m	Q9jr80 neisseria m

ALIGNMENTS

Q9UJZ1 PRELIMINARY; PRT; 356 AA.
Q9UJZ1;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MEMBRANE ASSOCIATED PROTEIN SLP-2 (STOMATIN-LIKE PROTEIN 2) (STOMATIN-LIKE 2) (CDNA FLJ14499 FIS, CLONE NTZRM100080, WEAKLY SIMILAR TO UNC-1 PROTEIN) (STOMATIN-LIKE 2).
HUSLP2 OR SLP2.

Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=HEART MUSCLE; Wang Y., Morrow J.S.; Wang Y., Morrow J.S.; Wang Y., Morrow J.S.; Norel Homologue "Identification and Characterization of Human SLP-2, a Novel Homologue of Stomatin (band 7.2b) Present in Erythrocytes and Other Tissues."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Owczarek C.M., Treutlein H.R.,
                                                                                                                           Strausberg R.;
Submitted (FEB-2001)
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                                           SEQUENCE FROM N.A.
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[sogai T.,
Ota T., Hayashi K.,
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Sugiyama T., Otsuki T., Suzuki Y.,
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Q96FY2;
01-DEC-2001 (TrEMBLrel. 19, C:
01-DEC-2001 (TrEMBLrel. 19, L:
01-DEC-2001 (TrEMBLrel. 19, L:
STOMATIN LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Magatsuma M., Hosolri T., Kaku Y., Kodalra H., Kondo H., Sugawara Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Matanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
"Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Strausberg
Submitted (
                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                  TISSUE-LUNG CARCINOMA;
                            SEQUENCE FROM N.A.
                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
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                                                                                                                                                                                                                                                                                                                                                                                         Similarity 95.3
11; Conservative
 (JUL-2001)
                                            KE ...
IS (Human).
Mettazoa; Chordata; C
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Last sequence update)
Last annotation updat
 EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                               Score 1646; DB 4;
Pred. No. 1.2e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARCINOMA;
                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                           PRT;
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                                                                                        Query Match
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Best Local S
Matches 340
                                                                                                                                                                                                          EMBL; AF161458; AAF29073.1; -.
InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
PRINTS; PR00721; STOMATIN.
SMART; SM00244; PHB; 1.
SEQUENCE 342 AA; 37145 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9P042;
Q9P042;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                          Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G., Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W., Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z., "Cloning and functional analysis of cDNAs with open reading frames 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells.";

Senome Res. 10:1546-1560(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC010152; AAH10152.1; -. SEQUENCE 356 AA; 38518 MW; 6FC0BF899E1919A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20499367; PubMed=11042152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                              17
                                                                                           Local Similarity les 330; Conserv
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                                                                                        91.3%;
nilarity 97.1%;
Conservative
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19,
                                                                                        Score 1613.5; DB
Pred. No. 1.4e-95;
3; Mismatches 4
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Last annotation updat
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Pred. No. 3.4e-97;
2; Mismatches 12,
                                                                                                                                                                                                               7958C0E3BDBE53E5 CRC64;
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Best Local S
Matches 332
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01-AUG-1998
01-AUG-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1998) to the EMBL/GenBank/DDBJ EMBL; AC004472; AAC07983.1; -. InterPro; IPR001107; Band_7. Pfam; PF01145; Band_7; 1. SMART; SM00244; PHB; 1. SMART; SM00244; PHB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

TISSUE-FIBROBLAST OR FORESKIN;

TISSUE-FIBROBLAST OR FORESKIN;

Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,

Lamerdin J.E., McCready P.M., Kyle A., Ramirez M., Stilwagen S.,

Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,

Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise

Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,

Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,

Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,

Carrage A. M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              060376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
    184
                                                194
                                                                                          124
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                                                                                                                                                                                                 QSLKEIVINVPEQSAVTLDNVTLQIDGYLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRS
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                                                                                   ELGKLSLDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVXESMQMQVGA
                                                                                                                                                                            QSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRS
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Pred. No. 5.1e
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Matches 322
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InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
PRINTS; PR00721; STOMATIN.
SMART; SM00244; PHB; 1.
SEQUENCE 353 AA; 38385 MW;
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0610038F01Rin.
Mus musculus (Mouse).
Mus mvota; Metazoa; Chordata;
heria; Rodentia;
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Q99JB2;
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                                                                                                                                                                                                                                                                                                                                PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS 356
                                                                                                     QAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILL
                                                                                                                                                                                        DIHVPPRVKESMOMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN
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                                                                                 QAAGEASAVLAKAKAKAEAIRILAGALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTVLL
                                                                                                                                                                  DIHVPPRVKESMOMQVEAERRKRATVLESEGTRESAINVAEGKKOAQILASEAEKAEQIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322;
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22; Conservative
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(TrEMBLrel. 17, Last sequence up
(TrEMBLrel. 19, Last annotation
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89.9%;
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Pred. No. 1e-90;
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Sciurognathi; Muridae;
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A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Mishi K., Kiyosawa H., Kasukawa T., Saito R.,
A A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                            Matches 320;
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O9DCG8
O1-JUN-2001 (TrEMBLrel 1
01-JUN-2001 (TrEMBLrel 1
01-JUN-2001 (TrEMBLrel 1
01-JUN-2001 (TrEMBLrel 1
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InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL: AK002793; BAB22363.1; ...
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                                                                                                                                                                                                                                                                                                                                      musculus (Mouse).
                                                                                                                                                                                                                                                                PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS
                                                                    QAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILL
                                                                                                                                          DIHVPPRVKESMOMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN
                                                                                                                                                                                              VEDPEYAVTQLAQTTMRSELGKLSLDKVFREREFLNANIVDAINQAADCWGIRCLRYEIK
                                                                                                                                                                                                                VEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIK 178
                                                   QAAGEASAVLAKAKAKAEAIRILAGALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTVLL
                                                                                                                         DIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /M N.A.
1/6J; TISSUE-KIDNEY;
85660; PubMed-11217851;
851bata K.,
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38530 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                               86.4%;
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17,
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1526.5;
Pred. No. 5.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D317CBB7E32F8863 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353
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T., Fukuda '
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                         238
                                                                                                                                                          238
                                                                                                                                                                                               178
                                                       298
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RA Harris N.L. Harvey D. Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L. Harvey D. Heiman T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Wenter E., Wang A.H., Wang X.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F. N., Ewin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster.";
DR FlyBase; FBgn0034936; CG2970.
DR FlyBase; FBgn0034936; CG2970.
DR FlyBase; FBgn0034936; CG2970.
DR FlyBase; PR00721; STOMATIN.
DR PARNTS; PR00721; STOMATIN.
DR PARNTS; PR00721; STOMATIN.
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Q9W1F7;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Borthan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunr
Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ammanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G. Wan K.H., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G. Natil J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., Andril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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CG2970.
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                  PRINTS; PR00721; STON SMART; SM00244; PHB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=10731132;
35668 MW;
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Last annotation update
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  D5C6241445FEF4DE CRC64
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Query Match Best Local Similarity

60.2%; 63.7%;

Score 1064.5; DB Pred. No. 1.6e-60;

DB 5;

Length

17;

Gaps

2

Conservative

55;

Mismatches

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OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OC COCO OCO    밁
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                                                                                                                                                                                                                                                                           Query Match 54.2%; Score 957.5;
Best Local Similarity 61.2%; Pred. No. 1.1
Matches 188; Conservative 58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        Science 282:2012-2018(1998).
EMBL; Z81072; CAB03018.1; -
InterPro; IPR001107; Band_7;
InterPro; IPR001972; Stomatin.
Pfam; PP01145; Band_7; 1.
PRINTS; PR00721; STOMATIN.
SMART; SM00244; PHB; 1.
SEQUENCE 334 AA; 36704 MW;
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O9XVP9;
O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F30A10.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99069613;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
    144
                                                  134
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AEQYIGAFKKLAKTNNTMILPSNPGDVNGFVAQALAVYNHVSNS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MFVPQQEAWVVERMGRFHRILDPGLNILVPVADKIKYVQSLKEIAIDVPKQSAITSDNVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQGTDA-----SXDEELDRVKMS
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Best Local Similarity
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O60121;
O60121;
O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 39.3 KDA PROTEIN C16G5.07C IN CHROMOSOME
SPBC16G5.07C.
Q93VP9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. SEQUENCE 354 AA; 39274 MW;
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SMART; SM00244; PHB; 1.
PROSITE; PS01270; BAND_7; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-1998) to the EMBL/GenBank/DDBJ-i-SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 EMBL; AL023554; CAA19027.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GVYGALT 320
                                                                                                                  VSLYIAQQYITNFGKLAKASNSMIVPASTSDVSGMVAQALSIFKQVSKTTAPDKSTPKEL
                                                                                                                                                            ASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTK--APVPGTPDSL
                                                                                                                                                                                                              INVAEGDKQAEILDSEGQKIKTINSALAEAQAIREKASATASGIAVLADSIKKQEHGLEA
                                                                                                                                                                                                                                            INVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAAL-TQHNGDAA
                                                                                                                                                                                                                                                                                                          IHITDAINKAAESWGIRCLRHEIRDIRPPESVVMAMHQQVSAERQKRAEILESEGKRQAA
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PRELIMINARY;
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  PRT;
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411
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Best Local S
Matches 168
Q9T082;
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EMBL; AY059109; AAL15215.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,

Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,

Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,

Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin Neumann G.,

Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.

Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,

Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O93VP9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
HYPOTHETICAL 45.0 KDA PROTEIN.
AT4G27580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ecker J.R., Theologis A.; "Full Length cDNA of gene AT4g27580 (GI:7269612)."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ datab
                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 411 AA; 4
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                                                                                                              ILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGAL 319
                                                                                                                                                                KRAQILESEGERQSHINIADGKKSSVILASEAAKMDQVNRAQGEAEAILARAQATAKGLV
                                                                                                                                                                            KRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIR
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                                                                                                                                                                                                                        KLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMOMQVEAERR
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            PRELIMINARY;
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; Pred. No. 3.8e
67; Mismatches
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            PRT;
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Best Local Similarity
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Q9LVW0;
Q9LVW0;
01-OCT-2000
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SEQUENCE FROM N.A.
Bevan M., Van Der Schueren J
Volckaert G., Hoheisel J., M
Volckaert G., Harander J
Van Der Schueren J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11-JUN-2001 (TrEMBLrel. 17, Last annotation update)
12-JUN-2001 (TrEMBLrel. 17, Last annotation update)
13-JUN-2001 (TrEMBLrel. 13, Created)
13-JUN-2001 (TrEMBLrel. 13, Created)
13-JUN-2001 (TrEMBLrel. 13, Created)
14-JUN-2001 (TrEMBLrel. 13, Created)
15-JUN-2001 (TrEMBLrel. 13, Created)
15-JUN-2001 (TrEMBLrel. 13, Created)
16-JUN-2001 (TrEMBLrel. 13, Created)
17-JUN-2001 (TrEMBLrel. 13, Last sequence update)
17-JUN-2001 (TrEMBLrel. 13, Last sequence update)
17-JUN-2001 (TrEMBLrel. 13, Last sequence update)
17-JUN-2001 (TrEMBLrel. 13, Last sequence update)
17-JUN-2001 (TrEMBLrel. 13, Last sequence update)
17-JUN-2001 (TrEMBLrel. 13, Last sequence update)
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17-JUN-2001 (TrEMBLrel. 13, Last sequence update)
17-JUN-2001 (TrEMBLrel. 13, Last sequence update)
17-JUN-2001 (TrEMBLrel. 13, Last sequence update)
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17-JUN-2001 (TrEMBLrel. 13, Last sequence update)
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17-JUN-2001 (TrEMBLrel. 13, Last sequence update)
18-JUN-2001 (TrEMBLrel. 13, Last sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein SEQUENCE 515 AA;
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Mayer K.F.X.;
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(MAR-1999) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 826; DB 10;
; Pred. No. 5.1e-45;
67; Mismatches 80
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Mewes H.W., Mayer K.F.X., Scl
e EMBL/GenBank/DDBJ databases
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Schueller
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Best Local Similarity
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InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
PRINTC: DDOCTOR
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILARITY TO SYOMATIN LIKE PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoniophyta; endicotyledons; core endicots; Rosid.
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            Ogata H., Audic S.,
Samson D., Roux V.,
Raoult D.;
                       MEDLINE-21442074; PubMed-11557893;
Ogata H., Audic S., Renesto-Audiffren
Samson D., Roux V., Cossart P., Weisse
                                                                                                                                                       HYPOTHETICAL PROTEIN RC0452 RC0452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00721; STOMATIN. SMART; SM00244; PHB; 1. SEQUENCE 401 AA; 43607
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                                                                 SEQUENCE FROM N.A. STRAIN=MALISH 7;
                                                                                                    Bacteria; Proteobacteria; alp Rickettsiaceae; Rickettsieae; NCBI_TaxID=781;
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                                                                                                                                           Rickettsia conorii.
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Nakamura Y., Kaneko T., Katoh T., Asamizu
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 evolution
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55.1%; Pred. No. 1.5e-44;
tive 58; Mismatches 72
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ch J., Claverie
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Best Local Similarity 54.4
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Best Local Similarity
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Q9ZDK0;
Q1-MAY-1999
Q1-MAY-1999
Q1-DEC-2001
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SMART; SM00244; PHB; 1.
Hypothetical protein; Complete
SEQUENCE 311 AA; 34040 MW;
                                                                                                                                                                                  EMBL; AJ235271; CAÀ14788.1; -. InterPro; IPR001107; Band_7. InterPro; IPR001972; Stomatin. Pfam; PF01145; Band_7; 1.
                                                                                                                                                                                                                                      mitochondria.";
Nature 396:133-140(1998).
                                                                                                                                                                                                                                                         MEDLINE=99039499; PubMed=9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete SEQUENCE 312 AA; 34025 MW;
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=MADRID E;
                                                                                                                                                                                                                                                                                                                                                            Rickettsiaceae;
NCBI_TaxID=782;
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EMBL; AE008609; AAL02990.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDN
VTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNAS
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                         MVKVVPQQQAWVVEKLGKFDKVLQPGLNLLIPIIQRVAYKHTLKEEAIDVTAQTAISNDN
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L 34.0 KDA PROTEIN.
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54.38;
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Pred. No. 2.2e-44;
                                                                                      Pred.
                                                                        red. No. 5e-44;
Mismatches 6
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F74F625EC567E5CA CRC64;
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A41878CAAABC49F5 CRC64;
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A Nadimpalli R., Yalpani N., Johal G.S., Simmons C.R.;

A Nadimpalli R., Yalpani N., Johal G.S., Simmons C.R.;

The prochibitins, Stomatins, and Plant Disease Response Genes Composed Prochibitins Superfemally that Controls Cell Proliferation, Ion Charles Composed Composed Composed Proceedings of the EMBL/GenBank/DDBJ databases.

The Regulation, and Death.";

EMBL; AF236372; AAF68388.1; -.

RembL; AF236372; AAF68388.1; -.

R InterPro; IPR001107; Band_7; 1.

R InterPro; IPR001972; Stomatin.

R Pfam; PF01145; Band_7; 1.

R Pfam; PF01145; Band_7; 1.

R PF1NTS; PR00721; STOMATIN.

R SMART; SM00244; PHB; 1.
                                                                                                                                                                                                                                                                                                              Query Match 45.0%; Score 794.5; DB 10; Length Best Local Similarity 47.0%; Pred. No. 3.7e-43; Matches 171; Conservative 63; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9M585 PRELIMINARY; PRT; 394 AA. Q9M585; 01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) STOMATIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
328 FVAQAMKTYEQIHSHSQALKSHPQIEELKESGETSPAPSSEASKTPPLIEEADSNQTFSL
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                                                                                                                                                          IVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAIN 216
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                                                                                                                       ESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAV 247
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Search completed: September 22, 2002, 18:30:03 Job time: 546 sec

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US-08-781-562-5
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Patent No. 5763589
                                                            Query Match 9.6%; Score 169; DB 1; Length 415; Best Local Similarity 23.1%; Pred. No. 2.2e-08; Matches 61; Conservative 53; Mismatches 120; Indels
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SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hillman, Jenni
APPLICANT: Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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CITY: Palo Alto
STATE: CA
40 FVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTL 99 | : | | | : | | : | | : | | : | | : |
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                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                           LENGTH: 415 amino
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                                                                                                                                   Query Match
Best Local Similarity
Thes 73; Conserve
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; MOLECULE TYPE:
US-08-279-270A-1
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INFORMATION FOR SEQ ID NO: 1:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/279,270A FILING DATE: Concurrently herewith CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: UT
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                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                     144 DKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIH------------
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ZIP: 77210
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                                                                     TAEGVALTVTGVAQVKIMTEKELLAVACEQFLGLNVQDIKNVVLQTLEGHLRSILGTLTV
EQIYQDRDQFAKLVREVAAPDVGRMGIEILSFTIKDVYDKVDYLSSLGKTQTAVVQRDAD 131
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                                                                                                                                                                                                                                                                                                                                               379 amino acids
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                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                   8.7%; Score 154; DB 1;
19.6%; Pred. No. 5.6e-07;
tive 54; Mismatches 108
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                                                                                                                                                                                         Length 379,
                                                                                                                                                       Indels 138;
                                                                                                                                                       Gaps
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US-08-781-562-3
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; LIBRARY: GenBank
; CLONE: 1591514
US-08-781-562-7
                                                                         US-08-781-562-3
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: GOli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                        ATTORNEY_AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415.855-0555
                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                           STRANL_
TOPOLOGY: 11...
IMMEDIATE SOURCE:
LIBRARY: Genbar
'COMF: 31069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/781,562 FILING DATE: Herewith
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530 PRIOR APPLICATION DATA:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3174 Po:
CITY: Palo Alto
                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.1%; Score 354.5; DB 1; al Similarity 38.5%; Pred. No. 3.9e-27; 67; Conservative 46; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA
                                                                                                                                                                                                 288 amino acids
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15.9%;
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Pred. No. 1e-19;
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                  Length 288;
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                                                   Best Local
Matches
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                                                                                       Query Match
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APPLICANT: Hillman, Jen
APPLICANT: GOLI, Surya
                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOTTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 RAKVIAAEG----EMNASRALKEASMVITESPAALQL 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 LSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRK 200
41 VPQQEAWVVERMGRE--HRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVT 98
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mes 73; Conservat
                                                                                                                                                        LIBRARY: GenBank
CLONE: 1065452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/781,562 FILING DATE: Herewith
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                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                    TYPE:
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STREET: 3174 Porter Drive
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                                                     Conservative
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                                                                                                                                                                                                                                single
                                                15.3%; Score 271; DB 1; L
27.5%; pred. No. 1.1e-18;
24. Mismatches 78;
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                                                   Indels 50;
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US-08-781-562-6
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                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION RUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHAX: 415-845-4166
   STRANL...
TOPOLOGY: linc...
IMMEDIATE SOURCE:
LIBRARY: Owl
LOWE: 79701
                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hillman, Jenniter L.
APPLICANT: GGli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US
FILING DATE: Herewith
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                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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o. 5763589
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                                                                                                            381 amino acids
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RESULT 3
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; Patent No. 5763589
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Best Local Similarity
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                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,562
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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ADDRESSEE: Incyte Pharmaceuticals,
                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hillman, APPLICANT: Goli, Sur
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                               TYPE: amino acid
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Pred. No. 2.9e-38;
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US-08-781-562-1
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 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIOM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,562
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                   TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acid
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0181
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                       TOPOLOGY: line
                                                                                                                                                                                                                                                                                    TELEPHONE: 415-855-0555
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                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
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CITY: Palo Alto
STATE: CA
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PCT-US94-01712-27
   Score 1763; DB 1;
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161;
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99US-0161993.
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Score 826; DB 21; Pred. No. 6.2e-64; 67; Mismatches 80;
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Pred. No. 4.5e-64;
7; Mismatches 80
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Pred. No. 4.5e
57; Mismatches
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AAG50184 standard; Protein; 411 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve (tissue growth, and in tissue repair, healing of burns, incisions, culcers, for treating osteoporosis, osteoarthritis, bone degenerative cc ulcers, for treating osteoporosis, osteoarthritis, bone degenerative cc disorders, or periodontal disease. Furthermore, (I) is also useful for cc qut protection or regeneration and treatment of lung or liver fibrosis, creperfusion injury in various tissues, various immune deficiencies and cc disorders including severe combined immunodeficiency (SCID), bacterial or cc fungal infections, autoimmune disorders e.g. multiple sclerosis, crhoumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic creactions and conditions, such as asthma or other respiratory problems. Cc in addition, (I) affects biorhythms or circadian cycles of rhythms, cc dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides co analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAUZ8020-AAUZ8395 represent novel human secreted protein composition acid sequences of the invention.
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Best Local S
Matches 242
                 Arabidopsis thaliana
                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                             Arabidopsis
                                                                                                                                                                         AAG20661 standard; Protein; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve
                                          termination
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                                                                                                                                                                                                                                                                                                                                                                                           vke----vxagmhgggqtggkratvlesegdptksasqlwqegkkqaqilaseaekaeq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                           thaliana
                                         sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.5%;
                                                                                           protein fragment SEQ ID
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Pred. No. 1.6e
20; Mismatches
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                                                     promoter;
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  16-JUN 1999
17-JUN 1999
18-JUN 1999
21-JUN 1999
22-JUN 1999
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05-MAR 1999
09-MAR 1999
23-MAR 1999
25-MAR 1999
20-MAR 1999
01-APR-1999
01-MAY-1999
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14-JUN-1999;
16-JUN-1999;
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VQGTDA-----SXDEELDRVKMS

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RESULT 1
AAU33158
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                                                                                                                                                                                                         cc determining the presence of or predisposition to a disease associated cc with altered levels of polypeptide. The polypeptides are also useful for cidentifying agents (agonists and antagonists) that bind to them. Cells cexpressing the proteins are useful for identifying a therapeutic agent (for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising cc the nucleic acids encoding the polypeptides and cells genetically crimine are useful in genetic vaccination, testing and therapeutic series are useful in genetic vaccination, testing and cc increase stem cell proliferation; to regulate haematopoiesis; and in the carpitaling the proteins and/or stimulation; as anti-inflammatory agents; and cc in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid cc sequences of novel human secreted proteins of the invention.
                                                                                                                     Query Match
Best Local
                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding a vaccination, testing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-APR-2000; 2000US-0552929
26-JAN-2001; 2001US-0770160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted protein #3649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU33158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU33158 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune suppression;
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                                                                                                                                                                                Sequence
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                                                                                                                     Local Similarity
                 59
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                                                                        1 MLARAARGHWGPFAEG--LSTGFWPRSGRASSGLPRNTVVLFVPQQEAWVVERMGRFHRI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates
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                 LEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYG
                                            mlaraargtgalllrgsllasgrapr--rassglprntvvlfvpqqeawvvermgrfhri
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HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 716; 765pp; English
                                                                                                                                                                                 222
                                                                                                       Conservative
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                                                                                                                     57.2%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           to novel human secreted polypeptides. The bodies to the polypeptides are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  range of human polypeptides, useful in genetic therapy - \mbox{}^{\phantom{\dagger}}
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                                                                                                       2:
                                                                                                                     Score 1011; DB 22; Pred. No. 1.1e-80;
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                                                                                                         Mismatches
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ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; plattelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
         The invention relates to novel isolated human secreted polypeptides (I) and plynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopolesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      severe combined immunodeficiency; SCID; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; arthritis; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human secretory protein,
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                                                                                                                                                                                                                                               Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders.
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                                                                                                                                                                                                                  Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                     20-OCT-2000;
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17-JUN-2000;
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Yang Y,
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2000US-0616847.
2000US-0665363.
2000US-0693267.
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2000US-0574454
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Drmanac |
                                                                                                                                                                                                                  No 598; 107pp; English.
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Huntington's
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Zhang J, Chen
   disease,
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neuropathy;
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АJ,
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Wang J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a fragment of a secreted human protein encoded by the nucleic acid molecule detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311.704410; maino acid sequences AAW78126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed (see AAX04311 for described mains the presence of the second of the described mains the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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                                                                                            DRVKMS
                                                                                                                                                                                                                        RMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIM 110
                                                                          drvkms
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N1 J,
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97US-0060841.
97US-0060844.
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97US-0061059.
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97US-0058972.
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Olsen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences (ABL01840 (ABB57737-ABB72072)
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DB; ABL03644.
                                     AEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRD
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynuclectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammanomodists regulating activity, tissue growth factor activity, hammanomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                              Sequence
                                                                                   Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                          The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elatic cytokine, cell proliferation or cell differentiation or which may inc
                                                                                                                                                                                                                                                                                                   Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
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                                                                                                                                      treatment of cancer, leukaemia, nervous system disorders, arthritis and
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Wang D,
Yang Y,
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2000US-0560875
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Wang J, Zhang J, Ren
Wejhrman T, Goodrich R
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             92.5%;
Score 1635; DB 22;
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13-JUN-1997;
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97US-0061060

97US-0049548

97US-0049549

97US-0049506

97US-0049607

97US-0049607

97US-0049608

97US-0049610

97US-0049611

97US-0050566

97US-0050566

97US-0050911

97US-005091

97US-005091

97US-005091

97US-005091

97US-005091

97US-005091

97US-005091
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Best Local Similarity
Matches 341; Conser
                    17-JUN-2000;
14-JUL-2000;
19-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                    ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombovytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammation.
Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                 07-MAR-2000;
19-MAY-2000;
                                                                                                   05-MAR-2001;
                                                                                                                                                 WO200166689-A2
                                                                                                                                                                                                                                                                                    Human; secreted
                                                                                                                                                                                                                                                                                                           Novel human
                                                                                                                                                                                                                                                                                                                                   18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                       AAU28053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                          13-SEP-2001
                                                                                                                                                                                            fertility; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       psnpgdvtsmvaqamgvygaltkapvpgtpdslssgssrdvqgtdasldeeldrvkms
                                                                                                                                                                                                                                                                                                                                                                                                                                              PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mlaraargtgalllrgsllasgrapr--rassglprntvvlfvpqqeawvvermgrfhri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAAGEASAVLAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dihvpprvkesmqmqveaerrkratvlesegtresainvaegkkqaqilaseaekaeqin
HYSEQ
                                                                                                                                                                                                                                                                                                                                                                              standard;
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                    2000US-0519705.
2000US-0574454.
2000US-0596193.
2000US-0616847.
2000US-0665363.
2000US-0693267.
                                                                                                                                                                                                                                                                                                         secretory protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                   2001WO-US04942
                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                  protein; arthritis; Crohn's disease; sepsis; shock;
                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.2%;
95.3%;
                                                                                                                                                                                          pain;
                                                                                                                                                                                             antigen
                                                                                                                                                                                                                                                                                                                                                                              3007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1646; DB 22;
Pred. No. 4.8e-136;
2; Mismatches 11;
                                                                                                                                                                                                                                                                                                        Seq
                                                                                                                                                                                                                                                                                                           ID No
                                                                                                                                                                                                                                                                                                           222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2111 (AAK52582) and 3666 from the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378;
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179 179 119 119 59 59 ب ш

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238

VEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIK 178

178

238

DIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN

dihvpprvkesmqmqveaerrkratvlesegtresainvaegkkqaqilaseaekaeqin

LEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYG

lepglnilipvldriryvqslkeivinvpeqsavtldnvtlqidgvlylrimdpykasyg

118

MLARAARGHWGPFAEG--LSTGFWPRSGRASSGLPRNTVVLFVPQQEAWVVERMGRFHRI

mlaraargtgalllrgsllasgrapr--rassglprntvvlfvpqqeawvvermgrfhri

58 58

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Matches

340;

Conservative

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Mismatches

Query Match Best Local Similarity

93.0%;

Score 1643; Pred. No. 1

DB 22; .5e-134;

Length 3007; Indels

4.

Gaps

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Sequence

3007

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cc sclerosis. In addition, (I) is involved in chemotactic or chemokinetic cartivity, regulation of haematopoiesis and is useful for treating myeloid cc or lymphoid cell disorders, platelet disorders such as thrombocytopenia cc and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, cc ulcers, for treating osteoporosis, osteoarthritis, bone degenerative cd disorders, or periodontal disease. Furthermore, (I) is also useful for cg gut protection or regeneration and treatment of lung or liver fibrosis, creperfusion injury in various tissues, various immune deficiences and cd disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, creations and conditions, such as asthma or other respiratory problems. Cc reactions and conditions, such as asthma or other respiratory problems. Cc reactions for the conditions, catabolism, anabolism, storage or elimination of distary fat, lipid, protein, carbohydrate, vitanins, minerals, provides condition in the condition of conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopolesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, parkinson's disease, Huntington's disease, and amyotrophic lateral
                                analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-589934/66.
N-PSDB; AAS44953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides and nucleic acids obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepared
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from various human tissues, neurological, inflammatory,
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Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID No 222; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , х t
, С,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relates to novel isolated human secreted polypeptides (I)
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Drmanac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Wehrman
Zhang J, Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , for diagnosis and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           m cDNA libraries s and treatment o e disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment of
orders -
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AJ,
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Wang J;
                                                              protein
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CC sequences ABABAYSA represent nucleic acids encoding them. The controlled of the invention and properties and recombinant host cells comprising a communication also relates to vectors and recombinant host cells comprising a communication and the nucleotide of the invention methods of detecting the nucleotides. CC antibodies against the polypeptides, methods of identifying compounds which comprising a compound of the invention although novel, many of the polypeptides of the invention have homology to known proteins, thereby compressive their probable biological activities, and hence content at the rapeutic applications. The polypeptides of the invention may competent at the rapeutic applications. The polypeptides of the invention may compound activities, including cytokine, cell proliferation or cell conditions activities; and proved in communomodulatory activity; activity; it is sue growth factor activity. CC immunomodulatory activities; and compound activities; or may be conditions or chemokinetic activities; haemostatic, thrombotic or chemokinetic activities; haemostatic, thrombotic or chemokinetic activities; haemostatic, thrombotic or chemokinetic activities; haemostatic, thrombotic or chemokinetic activities; receptor or ligand activities; or may be pepending on their biological activities; haemostatic, thrombotic or chemokinetic activities; receptor or ligand activities; or may be pepending on their biological activities, polypeptides and nucleotides of cc ancers, haematopietic disorders (e.g., volypeptides and nucleotides of cc cancers, haematopietic disorders (e.g., mathing or ameliorating medical cc activities; and proved in cell call disorders (e.g., pathoconditions include cell cancers, haematopietic disorders (e.g., osteoporosis), and abnormal cc arreal and fungal infections in addition to immune disorders.

Polypeptides with growth factor activity may be used to promote wound cc polypeptides may be used to conditions, and nucleotides autolimane disease or accidental damage. The polypeptides and n
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                                                                                                                                                            Query Match
Best Local S
Matches 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-FEB-2000;
27-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 291; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
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                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                 Local Similarity
    13
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                  LEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYG 118
                                                                                                MLARAARGHWGPFAEG--LSTGFWPRSGRASSGLPRNTVVLFVPQQEAWVVERMGRFHRI 58
lepglnilipvldriryvqslkeivinvpeqsavtldnvtlqidgvlylrimdpykasyg
                                                                              mlaraargtgalllrgsllasgrapr--rassglprntvvlfvpqqeawvvermgrfhri
                                                                                                                                                              341;
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                                                                                                                                                                                                                                                                                                                     techniques. The present sequence represents a novel human
                                                                                                                                                                                                                                                             378
                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0496914.
2000US-0560875.
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                                                                                                                                                                                                                                                                                                invention
                                                                                                                                                                               93.2%;
                                                                                                                                                            2,
                                                                                                                                                                               Score 1646; DB 22;
Pred. No. 4.8e-136;
                                                                                                                                                              Mismatches
                                                                                                                                                                                                   Length
                                                                                                                                                              Indels
                                                                                                                                                              4.
                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                              03-FEB-2000;
27-APR-2000;
20-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene vaccine; peptide therapy; stem cell growth factor; haematopoiesi tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-2001 (first entry)
         activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating
                                                                                                                                                                                                                                Zhao
                                                                                                                                                                                                                                                                                                                          01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM79550 standard; Protein; 378 AA.
                                                                                                                             Claim
                                                                                                                                                             Nucleic acids encoding polypeptides with cytokine-like activities
                                                                                                                                                                                                                                                                                                   15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                    Xue AJ,
                                                                                                                                                                                                                                                                 (HYSE-)
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                                                                                                                                                                                   2001-476283/51.
DB; AAK52683.
                                                                                                                            20; Page 281-282; 6221pp; English.
                                                                                                                                              in
                                                                                                                                                                                                                                                                HYSEQ INC
                                                                                                                                                                                                             Wang L.
                                                                                                                                                  diagnosis and
                                                                                                                                                                                                                                           Liu C,
                                                                                                                                                                                                                                                                                                                       2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
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2000US-0693325
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                                                                                                                                                                                                                    , Wang J,
Wejhrman
                                                                                                                                                                                                                  Drmanac RT, Asundi V,
Wang J, Zhang J, Ren
Wejhrman T, Goodrich R;
  leukaemia,
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  nervous
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  disorders,
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Wang
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7 ZW;
  arthritis and
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprisementary to the complementary strand of a polynucleotide which comprises of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence, where the
                                                                                                                                                                                                                                          Ota T,
Ishii
                                                                                                                                   Claim
                                                                                                                                                                     and/or
                                                                                                                                                        full-length
                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein sequence SEQ ID NO:11010
                                                                                                                                                                                                                                                                           (HELI-) HELIX RES
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3, Sugiyama
                                                                                                                                  SEQ ID 11010;
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; 2000JP-0183767.
; 2000JP-0241899.
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99JP-0300253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection; diagnosis; antisense therapy; gene therapy
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m T, Wakama
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Wakamatsu A,
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A, Nagai K,
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Otsuki
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299 299

PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS 356

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Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                       oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH3633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH3633 represent human amino acid sequences; and AAH3629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                 179
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   239
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                                                                                                                                                                                                                                                       l mlaraargtgalllrgsllasgrapr--rassglprntvvlfvpqqeawvvermgrfhri
                                                                                                                                                                                                                                                                           1 MLARAARGHWGPFAEG--LSTGFWPRSGRASSGLPRNTVVLFVPQQEAWVVERMGRFHRI
                                                                                                                                                                                                                                                                                                                                                            Match
                                                                                                                                             VEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIK 178
                                                                                                                                                                                       \tt dihvpprvkesmqmqveaerrkratvlesegtresainvaegkkqaqilaseaekaeqin
                                                                                DIHVPPRVKESMOMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN
                                                                                                                            356
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                         93.2%;
95.3%;
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                                                                                                                                                                                                                                                                                                                                           Score 1646; DB 22;
Pred. No. 4.4e-136;
                                                                                                                                                                                                                                                                                                                             Mismatches
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ABB11981
ID ABB11981 standard; peptide; 378 AA.
ID ABB11981;
XX
XX
XX
AC ABB11981;
XX
DT 11-JAN-2002 (first entry)
XX
XX
XX
XX
XX
Human SLP-2 homologue, SEQ ID NO:2351.
XX
XX
XX
Human; cytokine; cell proliferation; cell
XX
XX
XX
Human; cytokine; cell proliferation; cell
XX
XX
XX
Human; cytokine; cell proliferation; cell
XX
XX
XX
Whenatopolesis regulation; tissue growth
XX
XX
The control of the control of the cell disorder; tumonid cell disorder; tumonid cell disorder; tumonid cell disorder.
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolygsis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative rethnopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; ell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.

ID ACC XXX ACC

WO200157188-A2

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RESULT
AAW78160
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Query Match
Best Local S
Matches 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goli
                                                             Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative discrder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; ALDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt DNA} encoding human integral membrane protein -recombinant protein, for treatment of anaemia \epsilon
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                                                                                                                                                                             Human secreted
                                                                                                                                                                                                                                                             AAW78160 standard;
                                                    endocrine;
                                                                                                                                                                                                                                   AAW78160
                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                               NPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDEVKMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDI 180
                                                                                                                                                                                                                                                                                                                                                                                      dpeyavtqlaqttmrselgklsxdkvfrereslnasivdainqaadcwgirclryeikdi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 AA;
                                                    metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.8%; Score 1763; DB 19; ilarity 100.0%; Pred. No. 2.4e-146; Conservative 0; Mismatches 0;
                                                                                                                                                                            protein encoded by
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                                                                                                                                                                                                                                                               Protein;
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                                                   regulation;
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                                                                                                                                                                            gene 35 clone HTXCS21.
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WO9856804-A1

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1 MLARAARGHWGPFAEG--LSTGFWPRSGRASSGLPRNTVVLFVPQQEAWVVERMGRFHRI

Query Match
Best Local Similarity
Matches 341; Conser

Conservative

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Score 1646; DI Pred. No. 4.4e 2; Mismatches

; DB 20; 4.4e-136; nes 11;

Indels Length

4.

Gaps

2

58

356;

93.2%;

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13-JUN 1997
08-JUL 1997
18-AUG-1997
12-SEP-1997
02-OCT-1997
02-OCT-1997
02-OCT-1997
02-OCT-1997
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13-JUN-1997;
13-JUN-1997;
13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                      Brewer
Moore F
                             This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generat fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAXV4302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAXV4311-XV4410; amino acid sequences AAXV8126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypucleotides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed
                                                                                                                                                                                                                                  New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                            Claim 11; Page 282-283;
                                                                                                                                                                                                                                                                                       N-PSDB; AAX04345.
                                                                                                                                                                                                                                                                                                  WPI; 1999-080881/07
                                                                                                                                                                                                                                                                                                                           Yu GL;
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09-JUN-1998. 09-TAN-1007. 07115-0781569	US5763589-A.	Key Misc-difference 143 /label= unknown /note= "encoded by NTG" Misc-difference 173 Misc-difference 346 /label= unknown /note= "encoded by NTT"	t; pancreatic; tumour; ion transport.	al membrane protein.	03-AUG-1998 (first entry)	AAW57232;	ULT 1 57232 AAW57232 standard; Protein; 356 AA.	ALIGNMENTS	315 21 AAY75897 315 21 AAY75899	3 712.5 40.3 315 21 AAY75896	1 712.5 40.3 315 21 AAY75894	0 712.5 40.3 315 21 AAY75893	8 712.5 40.3 315 21 AAY75781	6 /12.5 40.3 315 21 AAB25626 7 712.5 40.3 315 21 AAY74991	5 712.5 40.3 315 21 ABS 8566	3 714.5 40.4 315 21 AAY75891 4 714 40.4 315 21 AAY75901	1 714.5 40.4 315 21 AAY75889 2 714.5 40.4 315 21 AAY75890	0 714.5 40.4 315 21 AAY75888	715 40.5 315 21 ANY 15000	6 716 40.5 315 21 AAY75783 7 716 40.5 315 21 AAY75886	4 716 40.5 315 21 AAY74992 5 716 40.5 315 21 AAY75780	3 716 40.5 315 21 AABZ36Z8	1 716 40.5 315 21 AAB3635 2 716 40.5 315 21 AAB35625	9 716 40.5 315 21 AAB5855	7 816.5 46.2 411 21 AAG48815 R 794 5 45 0 394 21 AAV84663	5 816.5 46.2 382 21 AAG48817 6 816.5 46.2 401 21 AAG48816	3 826 46.7 411 21 AAG50184 4 826 46.7 515 21 AAG31395	2 826 46.7 411 21 AAG20661
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Matches 26; Conserv
                                                                                                                                                  This sequence represents a fragment of a secreted human protein encoded by the nucleic acid molecule detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in a sample or which tissues they are most highly expressed in the new polynucleotides.
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18-AUG-1997;
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N-PSDB; AAX04345.
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Rosen CA, Ruben SM, Shi Y, Young P;
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Matches 27
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97US-0058669.
97US-0058750.
97US-0058971.
97US-0058972.
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97US-0049606.
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97US-0049549
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97US-0050566
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6.9e-19;
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RESULT 1
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Best Local S
Matches 26
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02-OCT-1997;
02-OCT-1997;
02-OCT-1997;
02-OCT-1997;
02-OCT-1997;
02-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW78287
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N-PSDB; AAX04345.
                                                                                                                                                                                                                                                                                          cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
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Ni J, Olsen
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                                                                                                                                                                                                                                                      regulation; malabsorption;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AM,
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n CA, Ruben SM, Shi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
, 6.3e-18;
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                                                                                                                                                                                                                                                      gastritis; neoplasm.
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                                                                                                                                                     cc ischaemia reperfusion injury, shock, sepsis, immune responses, and is is called in increasing haematopolesis, stem cell survival, bone growth can dremodeling. (I), (II) and modulators of (II) are useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve cancers (II) is also useful for the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve can derivity in tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, comparison's disease, Huntington's disease, and amyotrophic lateral cativity, regulation of haematopolesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia cativity, regulation of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, cultissue growth, and in tissue repair, healing of burns, incisions, cativity or periodontal disease. Purthemore, (I) is also useful for culters, for treating osteoporosis, osteoarthritis, bone degenerative conditions and treatment of lung or liver fibrosis, catebolism, anabolism, storage or elimination of constitions and treatment of lung or liver fibrosis, catebolism, catabolism, anabolism, storage or elimination of constity and can act as an antigen in a vaccine composition to raise an infection and can act as an antigen in a vaccine composition to raise an infection of the invention.
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14-JUL-2000;
19-SEP-2000;
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Zhao
                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; SEQ ID No 598; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -
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19-MAY-2000;
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      108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to novel isolated human secreted polypeptides
                 RASSGLPRNTVVLEVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYV 76
rassglprntvvlfvpqqeawvvermgrfhrilepglnilipvldriryv 157
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DB; AAS45141.
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2000US-0596193.
2000US-0616847.
2000US-0665363.
2000US-0693267.
                                                                     Conservative
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                                                               14.08; 5cc
100.08; P;
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                                                                                   Score; Pred.
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T, Zhang J,
                                                                    Mismatches
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                                                                                   DB 22; I
2.7e-40;
                                                                                                  Length 463;
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Brewer LA, Moore PA,

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J,

Olsen

Ferrie ,SH

Rosen ¥,

Feng P, Greene JM, n CA, Ruben SM, Shi

Lafleur DW; Y, Young P

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1999-080881/07. DB; AAX04345.

This sequence represents a fragment of a secreted human protein ence by the nucleic acid molecule detailed in the descriptor line. The can be used to generate fusion proteins by linking to the gene to a

n encoded The gene

gene

Disclosure; Page 35; 380pp; English.

New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders

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AAW78286
ID AAW7
08-JUL-1997
18-AUG-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymu osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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                                                                                                                                                            (HUMA-)
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13-JUN-1997
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13-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fragment of human secreted protein encoded by
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                                                                                                                                                                                                                                                                                                                                          13-JUN-1997
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                                                                                                                                                            HUMAN
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                                                                                                                                                            GENOME
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97US-0060844.
97US-0060865.
97US-0061059.
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97US-0058972
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97US-0058750
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
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Homo sapiens.
                            nervous
                                                                                              Human polypeptide
                                                                                                                           06-NOV-2001
                                                                                                                                                                                AAO09538 standard; Protein; 92 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccination, testing and therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                    peqsavtldnvtlqidgvlylrimdpykasygvedpeyavtqlaqttmrselgkls 142
                                                                                                                                                                                                                                                                                                                                                                       116;
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                          system
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                                                                                                                                                                                                                                                                                                                                                                                                                                            222
                                                                                                                                                                                                                                                                                                                                                                    32.6%; ilarity 100.0%; Conservative
                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą,
                            disorders; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            716; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT
                                                                                              SEQ ID NO 23430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      range of human polypeptides, useful in
                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                Score 116; DB 22;
Pred. No. 3.2e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human secreted polypeptides.
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                            inflammation.
                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                              Length 222;
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AAU28241
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity tissue growth factor activity, immunomodulatory activity and activinyinhibin activity and may be useful in the diagnosis and/or regiment of cancer lanksemia.
                                                                          Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                             Homo sapiens.
                                                                                                                                                                                                                               Novel human secretory protein, Seq ID No 598.
                                                                                                                                                                                                                                                                   18-DEC-2001
                                                                                                                                                                                                                                                                                                                                    AAU28241 standard; Protein; 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment of cancer, leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 23430; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2000;
18-MAY-2000;
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                                                             fertility; analgesic; pain; antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                        294 NTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDAS
                                                                                                                                                                                                                                                                                                                                                                                                                     30 ntillpsnpgdvtsmvaqamgvygaltkapvpgtpdslssgssrdvqgtdas 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to human polynucleotides (AAI79941-AAI93841) and
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100.0%;
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Pred. No.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoded polypeptides (AAM/8323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, hammomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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Zhao QA,
Xue AJ,
             Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopolesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemi
                                                                               Novel human
                                                                                                             18-DEC-2001
                                                                                                                                                                         AAU33159 standard; Protein; 2797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammation.
Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3656 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 3486-3487; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities useful in diagnosis and gene therapy -
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nes 298; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                        RASSGLPRNTVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINV 86
                                                                                                                                                                                                                                                                                                                                                                                          FRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLE 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKV 146
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Wang D, Wang J, Z
Yang Y, Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 AA;
                                                                           secreted protein
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                                                                                                           (first entry)
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                         AAU33158 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy - \,
                                                                 Novel human secreted protein #3649
                                                                                                      18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                       283 VSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSSRDVQGT 342
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                                                                                                                                                                                                                                                                                                                                       vsafsklakdsntillpsnpgdvtsmvaqamgvygaltkapvpgtpdslssgssrdvqgt 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.6%; Score 123; DB 22; ilarity 100.0%; Pred. No. 4.5e-111; Conservative 0; Mismatches 0.
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
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Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemi

В Ş

327 327

345 345

in

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8284
                                                                                                                                18-AUL-1997
118-AUC-1997
12-SEP-1997
02-OCT-1997
02-OCT-1997
02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoprosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
    useful
                                                               ĭu
                                                                        Moore PA,
                                                                                                                                                                                                                                                                    13-JUN-1997;
13-JUN-1997;
                                                                                                                                                                                                                                                                                                                    13-JUN-1997;
13-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fragment of human secreted
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                                                                                                    (HUMA-)
                                                                                                                                                                                                                                                                                        13-JUN-1997;
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13-JUN-1997
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  isolated human genes
ful for diagnosis and
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                                         1999-080881/07.
                                 AAX04345.
                                                                                 Ebner
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                                                                                                     GENOME
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970S-0058750
970S-0058971
970S-0058972
970S-0058875
970S-0060834
970S-0060841
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97US-0060865.
97US-0061059.
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97US-0049609.
97US-0049610.
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97US-0050566.
97US-0050901.
97US-0052989.
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97US-0049549.
97US-0049550.
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97US-0058668
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97US-0055984.
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                                                                        R, Fe
Olsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                     SCI INC
                                                                                 Ferrie
                                                                        ,SH
and the secreted polypeptides they encode treatment of e.g. cancers, neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein encoded by
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                                                                                 Ä,
                                                                        Rosen
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                                                                      Feng P, Greene JM,
n CA, Ruben SM, Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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                                                                      Lafleur DW;
Y, Young F
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RESULT
AAM78566
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Best Local S
Matches 202
03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a fragment of a secreted human protein encoded by the nucleic acid molecule detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed
                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; lander, rancor; la
                                                                                                                                                                                                           05-FEB-2001;
                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein
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les 202; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                        2000US-0496914.
2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0663561.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
     2000US-0693325
                                                                                                                                                                                                                                                                                                                                                                                                           factor; immunomodulatory; cancer;
n disorder; arthritis; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO
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100.0%; Pred. No. 2.6e-189;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358
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Best L
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                                07-MAR-2000; 2000US-0519705.
19-MAY-2000; 2000US-0574454.
17-JUN-2000; 2000US-0596193.
14-JUL-2000; 2000US-0616847.
19-SEP-2000; 2000US-0665363.
                                                                                                                                                                                                            gut protection; lung; liver fibrosis; immune deficiency; info
severe combined immunodeficiency; SCID; autoimmune disorder;
multiple sclerosis; rheumatoid arthritis; diabetes mellitus;
                                                                                                                                                                                                                                   ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer; disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammation.
Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                        05-MAR-2001;
                                                                                                                                13-SEP-2001
                                                                                                                                                      WO200166689-A2.
                                                                                                                                                                               Homo
                                                                                                                                                                                                     fertility; analgesic;
                                                                                                                                                                                                                                                                                                                          Novel human
                                                                                                                                                                                                                                                                                                                                                                         AAU28053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RASSGLPRNTVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINV 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peqsavtldnvtlqidgvlylrimdpykasygvedpeyavtqlaqttmrselgklsldkv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rassglprntvvlfvpqqeawvvermgrfhrilepglnilipvldriryvqslkeivinv 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity
318; Conser
                                                                                                                                                                                                                                                                                                 secreted protein; arthritis; Crohn's disease; sepsis;
HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                         secretory protein,
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                                                                                                        2001WO-US04942
                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.2%;
99.7%;
                                                                                                                                                                                                     pain; antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 218; DB 22; L
Pred. No. 6.9e-205;
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from
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                                                                                                                                                                                                                         allergy;
                                                                                                                                                                                                                                                                                                 shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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326

266 206 206

SEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALT

segtresainvaegkkqaqilaseaekaeqinqaageasavlakakakaeairilaaalt

147 147

87 87

PEOSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKV 146

FRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLE

frereslnasivdainqaadcwgirclryeikdihvpprvkesmqmqveaerrkratvle

RASSGLPRNTVVLFVPQQEAWVVERMGREHRILEPGLNILIPVLDRIRYVQSLKEIVINV 86

27 27 Query Match Best Local S Matches 318

Similarity

61.2%; 99.7%;

Conservative

0; Score Pred.

Mismatches

218; DB 22; No. 4.5e-204;

Length 3007;

0

Gaps

0;

Sequence

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disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoparthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and in the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopolesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, parkinson's disease, Huntington's disease, and amyotrophic lateral in the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the
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Zhao
                                                                           Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment cancer, neurological, inflammatory, and autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to novel isolated human secreted polypeptides
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DB; AAS44953.
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Drmanac
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Chang J, Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R
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АJ,
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Wang
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ing J;
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                                                                                                                                                                                                                                                                                                          CC thrombolytic activities; receptor or ligand activities; or may be convolved in oncogenesis, cancer cell proliferation or metastasis. CC Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical cc cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cc disorders), chronic inflammatory conditions (e.g., asthma or arthritis), cc proliferative retinopathy, atherosclerosis, coronary heart disease, cc arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal cc vascular growth. Polypeptides involved with tissue regeneration and cc immunomodulatory activities may be used to promote wound chealing (e.g., of burns, incisions and ulcers), while those with cc immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.

CC polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to cautoimmune disease or accidental damage. The polypeptides and nucleotides cautoimmune disease or accidental damage. The polypeptides and nucleotides cautoimmune disease or accidental damage. The polypeptides and nucleotides collypeptide of the invention.

CC polypeptide of the invention.
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Best Local s
Matches 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of identifying compounds which bind to polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g. arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
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27-APR-2000; 2000US-0560875.
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      109
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318;
                                                                                                                                                                                        Similarity
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                                                                                                                                                                     Conservative
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                                                                                                                                                                                        61.2%;
99.7%;
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                                                                                                                                                                                        Score 218; DB 22; Pred. No. 6.9e-205;
                                                                                                                                                                     Mismatches
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20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2001
e.g. stem cell growth ractor activity, mamma-version tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                  The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
                                                                                                                                                                                                                            Xue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein SEQ ID NO 3196
                                                                                                                                                                                                                                                                                                                                                                             03-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                    05-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                 Claim
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                                                                                                                                                                  Nucleic acids encoding polypeptides with
                                                                                                                                                                                                                                        Zhao
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30-NOV-2000;
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                                                                                                                                                                                                                                                                        (HYSE-)
                                                                                                                                                                                                                                                                                                                      15-SEP-2000;
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                                                                                                                                                                                          2001-476283/51.
DB; AAK52683.
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                                                                                                                                 20; Page 281-282; 6221pp;
                                                                                                                                                                                                                                                                        HYSEQ INC
                                                                                                                                                                                                                          Wang D,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein; 378 AA.
                                                                                                                                                        diagnosis and gene therapy
                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                          2000US-0560875.
2000US-0598075.
2000US-0620325.
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2000US-0693325
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Wang J, Zh
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Chang J, Ren
Goodrich R;
                                                                                                                                 English
                                                                                                                                                                    cytokine-like activities,
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide compristing a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to polynucleotide which comprises a 5'-end sequence which complementary to polynucleotide which comprises a 3'-end sequence, where the
                                                                                                                                                                                                                                                                                                                         29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                         Claim
                                                                                                                                                                                                                                                               Ota T,
                                                                                                                                                                full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
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                                                                                                                                         8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein sequence SEQ ID NO:11010
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                                                                                                                                                                                                                                                                                      HELIX RES
                                                                                                                                         SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                   Sugiyama
                                                                                                                                                                                                                                                                                                             99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                        ID 11010;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                   Η,
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                                                                                                                                      CD ROM;
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                                                                                                                                                                                                                                                             Hayashi K,
                                                                                                                                                                                                                                                   Nagai K,
                                                                                                                                      English
                                                                                                                                                                                                                                                             Saito
                                                                                                                                                                                                                                                Saito K,
Otsuki
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..
                                                                                                                                                                                                                                                             Yamamoto
                                                                                                                                                                         detection by the
                                                  combination
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RESULT
ABB11981
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Best Local
                                                                                                                         cytostatic; antifungal;
                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarthritic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibaccytostatic; osteopathic; vasotropic; cardiant; virucide; osteopathic; vasotropic; cardiant; virucide; vasotropic; osteopathic; vasotropic; vasotropic; vasotropic; vasotropic; vasotropic; vasotropic; vasotrop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human SLP-2 homologue, SEQ ID NO:2351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB11981 standard; peptide; 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rassglprntvvlfvpqqeawvvermgrfhrilepglnilipvldriryvqslkeivinv 86
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                                                                                                                               vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                  antiulcer
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Pred. No. 6.5e-205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 356;
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                                                                                                                                                        antibacterial;
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Homo sapiens

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RESULT

AAW78160

ID AAW7

XX AAW7

AC AAW7

XX AAW7

XX AWW

DT 13-A

XX Huma

XX Huma

XX Huma

XX diag

KW diag

KW inmu

KW inmu

KW inmu

KW inmu

KW inmu

KW ooste

KW ooste

KW endo

XX Homo

XX Homo

XX Homo
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                    Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; lumune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzhelmer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents human integral membrane protein (IMP). IMP may be administered to a subject to treat disorders associated with abnormal ion transport or membrane conductance as well as a variety of tumours, e.g. haemolytic anaemias and prostate, breast and pancreatic tumours. A vector capable of expressing IMP, or a fragment or a derivative thereof, may also be administered to a subject to treat the haemolytic anaemias and prostate, breast and pancreatic tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding human integral membrane protein - useful for recombinant protein, for treatment of anaemia and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                             Human secreted protein encoded by gene 35 clone HTXCS21.
                                                                                                                                                                                                                            13-APR-1999
                                                                                                                                                                                                                                                                                    AAW78160 standard; Protein;
                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                        241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEXAEQINQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1998-347418/30
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                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hvpprvkesmqmqveaerrkratvlesegtresainvaegkkqaqilaseaekaeqinqa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pglnilipvldriryvqslkeivinvpeqsavtldnvtlqidgvlylrimdpykasygve
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                                                                                                                                                                                                                           (first entry)
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Pred. No.
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WO9856804-A1.

Qy

27 RASSGLPRNTVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINV

Query Match Best Local Sim Matches 318;

Similarity

61.2%; 99.7%;

Score 218; Pred. No. 6.

DB 20; 5.5e-205; nes 1;

Length Indels

0;

0

Conservative

0;

Mismatches

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12-SEP-1997;
12-SEP-1997;
12-SEP-1997;
12-SEP-1997;
12-SEP-1997;
02-OCT-1997;
02-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUL-1997;
18-AUG-1997;
12-SEP-1997;
                                  portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino'acid sequences AAW78126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in the conditions of the second polynucleotides.
                                                                                                                                                                                                                                             New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                  This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc
                                                                                                                                                                                                                                                                                                    N-PSDB; AAX04345.
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Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                  02-OCT-1997;
02-OCT-1997;
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                                                                                                                                                                                                                     Claim 11; Page 282-283; 380pp; English.
                                                                                                                                                                                                                                                                                                                WPI; 1999-080881/07
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Sequence
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                                                                                                                                                                                                                                                                                                                                          GL;
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                         AAX04311
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Ni J, Olsen
                         for described uses).
                                                                                                                                                                                                                                                                                                                                                                                            GENOME
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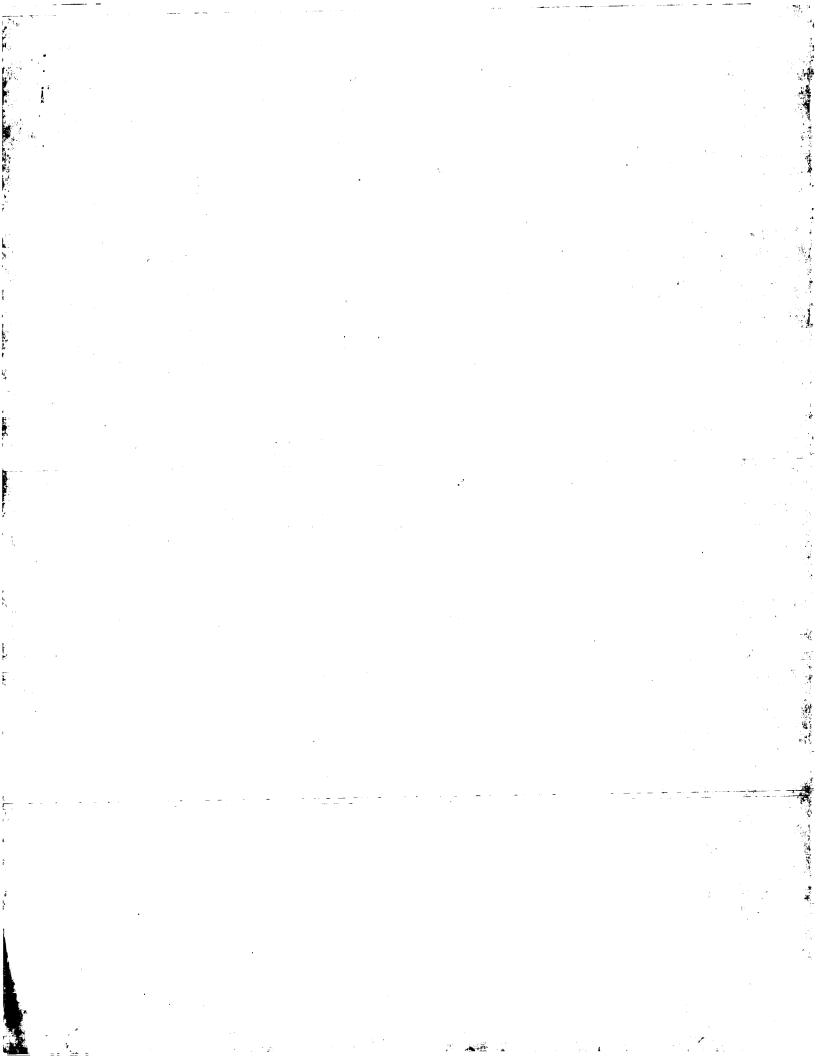
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EMBL; AJ235271; CAA14788.1;

InterPro; IPR001107; Band_7.

InterPro; IPR001972; Stomatin.

Pfam; PF01145; Band_7; 1.

PRINTS; PR00721; STOMATIN.

SMART; SM00244; PHB; 1.

SMART; SM00244; PHB; 1.

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MEDLINE=99039499; PubMed=9823893;
Andersson J.O.,
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A. S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of
mitochondria.";
   Rickettsia
                                                                    HYPOTHETICAL
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F74F625EC567E5CA CRC64;
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Submitted (MAY-1998) to the EMBL/GenBa-
-i- SIMILARITY: BELONGS TO THE BAND 7
-EMBL; AL023554; CAA19027.1; -
-InterPro; IPR001107; Band_7.
-InterPro; IPR001972; Stomatin.
-Pfam; PF01145; Band_7; 1.
-SMART; SM00244; PHB; 1.
-SMART; SM00244; PHB; 1.
                                                                                                                                                                                                                                                                                                                                            O60121 PRELIMINARY; PRT; 354 AA.
O60121;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
HYPOTHETICAL 39.3 KDA PROTEIN C16G5.07C IN CHROMO
SPBC16G5.07C.
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STRAIN-MALISH 7;
MEDLINE-21442074; PubMed-11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fo
Samson D., Roux V., Cossart P., Weissenbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; SEQUENCE 312 AA; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mechanisms of evolution in Rickettsia Science 293:2093-2098(2001).
                                                                                                       PROSITE; PS01270; BAN
Hypothetical protein.
SEQUENCE 354 AA; 3
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Schizosaccharomyces.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
PRLNTS; PR00721; STOMATIN.
SWART; SW00244; PHB; 1.
SEQUENCE 401 AA; 43607 MW; 2
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01-OCT-2000
01-OCT-2000
                                                   Q93VP9 PRELIMINARY; PRT;
Q93VP9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last annotype)
01-DEC-2001 (TrEMBLrel. 19, Last annotype)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILARITY TO STOMATIN LIKE PROTEIN.
Arabidopsis thaliana (Mouse-ear cres).
Eukaryota; Viridiplantae; Streptcophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE-20181125; Pubmed-10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Regulation, and Death.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF236372; AAF68388.1;
InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
PRINTS; PR00721; STOMATIN.
SMART; SM00244; PHB; 1.
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clones. 7:31-63(2000)
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Volckaert
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O9T082;
O1-MAY-2000 (TrEMBLrel. 13,
O1-MAY-2000 (TrEMBLrel. 13,
O1-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida Jones T., Kamiya A., Karlin Neumann G., Kawai J., Kim C., Koesema Lam B., Lin J., Meyers M.C., Miranda M., Nazusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "Full Length cDNA of gene AT4927580 (GI:7269612)."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY059109; AAL15215.1; -. EMBL; AY059124; AAK152431.1; -.
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SEQUENCE FROM N.A.

Sequence From N.A.

Banno F., Chang E., Dale J.M., Goldsmith A.D.,

Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,

Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,

Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,

Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,

Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,

Full Length CDNA of gene AT4q27580 (GI:7269612).";

"Full Length CDNA of gene AT4q27580 (GI:7269612).";
                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; wagnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL 55.9 KDA PROTEIN. T29A15.70 OR AT4G27580.
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                                                            Robben J.,
Mayer K.F.
                                                                                                                                                                                                                                     SEQUENCE FROM
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SEQUENCE 411 AA; 4
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13; Conser
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Van Der Schueren J., Chuang Y-J., Voet M.,
G., Hohelsel J., Mewes H.W., Mayer K.F.X.,
(MAR-1999) to the EMBL/GenBank/DDBJ databas
                                                                                                                          opsis sequencing project;
(MAR-1999) to the EMBL/G
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                                                                          Volckaert G,
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0.00038;
hes 0;
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edons; core eudicots; Rosidae;
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01-MAY-2000
01-JUN-2001
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;
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Ephydroidea; Drosophi
NCBI_TaxID=7227;
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                                              InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
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    PF01145;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
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PRINTS; PR00721; STOMATIN.
SMART; SM00244; PHB; 1.
SEQUENCE 334 AA; 36704 MW: 1.
                                                                             O9M585;
01-OCT-2000 (TrEMBLrel. 15, C:
01-OCT-2000 (TrEMBLrel. 15, L:
01-JUN-2001 (TrEMBLrel. 17, L:
CTOMATIN-LIKE PROTEIN.
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Barlow K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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InterPro; IPR001107; Band
InterPro; IPR001972; Stom
                                             Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnoliophyta;
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                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=99069613;
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SEQUENCE FROM N.A.
Nadimpalli R., Yalpani N.,
                           NCBI_TaxID=4577;
                                      Panicoideae;
                                                                 Zea mays (Maize)
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                                      Andropogoneae;
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                                                Streptophyta; Embryophyta; Tracheophyta;
/ta; Liliopsida; Poales; Poaceae; PACC clade;
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s; Pred. No. 3.
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thes 0;
 Simmons C.R.;
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A Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,

A Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,

A Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;

"Cloning and functional analysis of cDNAs with open reading frames for

"Cloning and functional analysis of cDNAs with open reading frames for

"Cloning and functional analysis of cDNAs with open reading frames for

"Stem/progenitor celis.";

"Stem/progenitor celis.";

"Stem/progenitor celis.";

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Best Local Similarity
Matches 143; Conserv
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Q9DCG8;
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01-JUN-2001 (TrEMBLrel. 1:
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061003BF01RIK PROTEIN.
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Q9P042;
Q1-OCT-2000
01-OCT-2000
01-DEC-2001
SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-KIDNEY;

MEDLINE-2108560; PubMed-11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-BLOOD,
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Pred. No. 1.7e-132;
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Best Local Similarity
                                                                              STRAIN-FVB; TISSUE-KIDNEY;
Chang J.G., Chan W.L.;
"Mouse stomatin-like protein 2 (MSLP2) mRNA.";
"Mouse stomatin-like protein 2 (MSLP2) mRNA.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ dai
EMBL; BC003425; AAH03425.1; -
EMBL; BC003425; AAH03425.1; -
EMBL; AF323178; AAG53404.1; -
EMBL; AF323178; AAG53404.1; -
MGD; MGI:1913842; 0610038F01Rik.
InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
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O99JB2;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last seq
O1-DEC-2001 (TrEMBLrel. 19, Last ann
RIKEN CDNA 0510038F01 GENE (STOMATIN
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Nature 409:685-690(2001)
EMBL; AK002793; BAB22363.1; -.
MGD; MGI:1913842; 0610038F01Rik.
InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
PRINTS; PR00721; STOMATIN.
SMARR; SM00244; PHB; 1.
PRINTS; PR00721; STOMATIN.
SMART; SM00244; PHB; 1.
SEQUENCE 353 AA; 38385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Wagatsuma M., Hosoiri T., Kaku
Takahashi M., Chiba Y., Ishida
Watanabe S., Kimura K., Murakar
Yamamoto J., Wakamatsu A., Nak
Ninomiya K., Iwayanagi T.,
"NEDO human cDNA sequencing pr
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EMBL; BC002442; BAB55091.1; --
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InterPro; IPR001107; Band_7; InterPro; IPR001107; Band_7; InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
PRINTS; PR00721; STOMATIN.
SMART; SM00244; PHB; 1.
SEQUENCE 356 AA; 38534 MW; 6
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01-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-DEC-2001 (TrEMBLrel. 19, L
STOMATIN-LIKE 2.
TISSUE=LUNG CAR
Strausberg R.;
Submitted (JUL-
                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi
Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1998) to the EMEL; AC004472; AAC07983.1; -.
InterPro; IPR001107; Band_7.
Pfam; PP01145; Band_7; 1.
SMART; SM00244; PHB; 1.
SEQUENCE 357 AA; 38749 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W., Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen Phan H., Velasco N., Garnes J., Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andr Trankhein M., Amico-Keller G., Coefield J., Duarte S., Lucas S Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae.
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060376;
01-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-FIBROBLAST OR FORESKIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; NCBI_TaxID=9606;
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                                         GVYGALTKAPVPGTPDSLSSGSSRDVQGTDAS
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Pred. No. 1e-190;
                                                                                                                                                                                                                                                                                              Score 152; DB 4; Le Pred. No. 2.3e-141;
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5: sp_inverteb:*
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Copyright (c) 1993 - 2000 Com
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sp_unclassified:*
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                      Q9m585 zea mays (m
Q9lrw0 arabidopsis
Q93wp9 arabidopsis
Q91082 arabidopsis
Q9zdk0 rickettsia
Q9zid8 rickettsia
Q9zid8 rickettsia
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Q96fy2
Q60376
Q9p042
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Q99jb2 mus musculu
Q9w1f7 drosophila
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Q9xvp9 caenorhabdi
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Q9UJZ1 PRELIMINARY; PRT; 356 AA.
Q9UJZ1;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MEMBRANE ASSOCIATED PROTEIN SLP-2 (STOMATIN-LIKE PROTEIN 2) (STOMATIN-LIKE 2) (CDNA FLJ14499 FIS, CLONE NTZRM100080, WEAKLY SIMILAR TO UNC-1 PROTEIN) (STOMATIN-LIKE 2).
HUSLP2 OR SLP2.

Q9csj6 mus musculu	Q9CSJ6	11	142	2.0	7	Ü
Q9ihw7 human immun	Q9IHW7	15	137		7	4
Q92ww3 rhizobium m	Q92WW3	16	136	•	7	w
Q9ybj8 aeropyrum p	8rayeo	17	135		7	N
Q9txe2 chlamys nip	Q9TXE2	σ	135	٠	7	1
088728 mus musculu	088728	11	134	•	7	0
Q939r0 fibrobacter	Q939R0	N	133	2.0	7	ف
rhizobium	Q98AP9	16	129		7	ão
Q9yc53 aeropyrum p	Q9YC53	17	121		7	7
Q26834 trypanosoma	Q26834	رى د	120		7	õ
Q9zj64 helicobacte	Q9ZJ64	16	112		7	σ̈
026072 helicobacte	026072	16	112		7	4
7	Q9APJ7	N	110		7	ω
Q9i0s4 pseudomonas	091054	16	95		7	Ñ
Q26830 trypanosoma	Q26830	ر.	95		7	į,
_	Q28882	σ	47	2.0	7	Ö
	Q53840	2	8817	•	œ	9
Q9vpr0 drosophila	Q9VPR0	ഗ	1443		œ	æ
Q9ned3 leishmania	Q9NED3	Ç,	754		8	7
O80256 vibrio chol	080256	ဖ	716		8	ŏ
	Q18703	ű	658		8	Ğ
	Q9VTX7	Çī	554		8	4
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062022 caenorhabdi	062022	ഗ	477		8	ລັ
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	Q9HXE1	16	263		80	ö
4	Q9A8D4	16	248		8	9
	Q94M69	9	235		œ	œ
077376 plasmodium	077376	5	374	٠	9	7

ALIGNMENTS

RA	RP	RN	RL	RA	RC	RP	RN	RL	RT	RT	RT	RA	RA	RC	RP	RN	RL	RT	RT	RA	RC	RP	RN	o x	8	8	SO	
ISOGAI T. Ota T. Havashi K. Sugivama T. Otsuki T. Suzuki Y.	SEQUENCE FROM N.A.	[4]	Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.	Strausberg R.;	TISSUE=LUNG CARCINOMA, SKIN, AND MELANOTIC MELANOMA.;	SEQUENCE FROM N.A.	[3]	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.	chromosome 9p13.1.";	protein 2 (SLP2), is ubiquitously expressed and localizes to HSA	"A novel member of the stomatin/EPB72/MEC-2 family, stomatin-like	Hertzog P.J.;	Owczarek C.M., Treutlein H.R., Portbury K.J., Gulluyan L.M., Kola I.,	TISSUE-BRAIN;	SEQUENCE FROM N.A.	[2]	Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	of Stomatin (band 7.2b) Present in Erythrocytes and Other Tissues.";	"Identification and Characterization of Human SLP-2, a Novel Homologue	Wang Y., Morrow J.S.;	TISSUE=HEART MUSCLE;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	

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                                                                                                                                            Matches
                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Jarvik
                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (619) 654-2428 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/762
FILING DATE: 09-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brotman, Harris F.
REGISTRATION NUMBER: 35,461
                                                                                                                                                                                                                                                 MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 516 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jarvik, Jonathan TITLE OF INVENTION: READING TITLE OF INVENTION: TAGGING
                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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   303
                                   113 YKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRC 172
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CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Harris Brotman STREET: 202 Coast Blvd., Suite 111
                                                                                                   FHRILEPGLNILIPVLDRIR--YVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDP 112
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L----VED---AAAALAAN--RSTLA------DKAASTAATVDA-----WAERQ 336
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                                                                      FDRLVSSGY-IYDPVMREVETAFMPWLKEQAIGYLAR------GVVARRVVDK 302
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                                                                                                                                            Conservative
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                                                                                                                                        5.9%; Score 104.5; DB 2; 25.6%; Pred. No. 0.067; ative 33; Mismatches 95;
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RESULT 10
US-09-320-774-8
: Sequence 8, Application US/09320774
; Patent No. 6265545
; GENERAL INFORMATION:
; APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: READING FRAME
; TITLE OF INVENTION: TAGGING
; TITLE OF INVENTION: TAGGING
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Best Local Similarity
"~+~hes 74; Conserva
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; ORGANISM: Chlamydomonas
US-08-745-404-2
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LENGTH: 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: Method For Producing Tagged of TITLE OF INVENTION: Method For Producing Tagged of TITLE OF INVENTION: Transcripts And Proteins FILE REFERENCE: 2087-961422
CURRENT APPLICATION NUMBER: US/08/745,404B
CURRENT FILING DATE: 1996-11-08
EARLIER APPLICATION NUMBER: 08/000,619
EARLIER FILING DATE: 1993-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 FDRLVSSGY-IYDPVMREVETAFMPWLKEQAIGYLAR-------GVVARRVVDK 302
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                                                                                                                                                                                                                                                                 -----EAVPKPPVKEVTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AKME-----AELQGKELEAVRRRPTFVĹRELKPAVASADAVEAA--AAELTAQAE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L-----VED---AAAALAAN--RSTLA------DKAASTAATVDA-----WAERQ 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.9%; Score 104.5; DB 25.6%; Pred. No. 0.067;
                                               Jonathan W.
READING FRAME INDEPENDENT EPITOPE
TAGGING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Mismatches
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ADDRESSEE: STREET: 2

3: Harris Brotman 202 Coast Blvd.,

Suite 111

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                                                                                                                                                                                                                                                                                                                  US-08-762-106-9
                                                                                                                                                                                 Sequence 9, Application US/08762106
Patent No. 5948677
GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: READING FRAN
TITLE OF INVENTION: TAGGING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 5.9%; Score 104.5; DB 4; Best Local Similarity 25.6%; Pred. No. 0.067; Matches 74; Conservative 33; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 516 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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ATTORNEY/AGENT INFORMATION:
NAME: Brotman, Harris F.
REGISTRATION NUMBER: 35,461
COMPUTER READABLE FORM
                                                                                                                                          NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                      442 ------LPDGVEPVDVEAEVAKAV---EAVPKPPVKEVTD 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 LRYEIKDIHVPPRVKESMOMOVEAERRKRATVLE-----SEGTRESAINVAEGKKOAO 225
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                     COUNTRY: U
                                                           ADDRESSEE: Harris Brotman
STREET: 202 Coast Blvd., (
CITY: La Jolla
STATE: California
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CLASSIFICATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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: California
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                                                                                                    Suite 111
                                                                                                                                                                                                           FRAME INDEPENDENT EPITOPE
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US-09-320-774-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/320,774 FILING DATE:
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REGISTRATION NUMBER: 35,461
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jarvik, Jonathan TITLE OF INVENTION: READING TITLE OF INVENTION: TAGGING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
LENGTH: 527 amino acid
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                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           453 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 EAANAKWEADKAEAAEKARAEAEAAAAEEQKALLEELAATAAAEAEERGEEPPAEPPS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 ILAS---EAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQY 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 LRYEIKDIHVPPRVKESMQMQVEAERRKRATVLE-----SEGTRESAINVAEGKKQAQ 225
                                                                                                                                                                                                               STREET: 202 Coast CITY: La Jolla STATE: California
CLASSIFICATION:
                                                                                                                                                                          COUNTRY: UZIP: 92037
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Local Similarity 25.6%;
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COMPUTER: II
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202 Coast Blvd., Suite 111
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SYSTEM: PC-DOS/MS-DOS
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                                     us/09/320,774
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                                                                                                                                                                                                                                                                                                                                                           FRAME INDEPENDENT EPITOPE
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/762,106
FILING DATE:

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                                                                                                                                                                                          ; LENGTH: 552
; TYPE: PRT
; ORGANISM: Chlamydomonas
US-08-745-404-3
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US-08-745-404-3
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                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: Method For Producing Tagged Genes,
TITLE OF INVENTION: Transcripts and Proteins
FILE REFERENCE: 2087-961422
CURRENT FILING DATE: 1996-11-08
EARLIER APPLICATION NUMBER: 08/000,619
EARLIER FILING DATE: 1993-01-05
EARLIER FILING DATE: 1993-01-05
                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08745404B Patent No. 6096717
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TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 654-2428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TYPE: amino acid
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Local Similarity 25.6%; Pred. No. 0.069;
hes 74; Conservative 33; Mismatches 95; Indels 87
                                     55 FHRILEPGLNILIPVLDRIR--YVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDP 112
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                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKME-----AELQGKELEAVRRRPTFYLRELKPAVASADAVEAA--AAELTAQAE 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRYEIKDIHVPPRVKESMQMQVEAERRKRATVLE-----SEGTRESAINVAEGKKQAQ 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FHRILEPGLNILIPVLDRIR -- YVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDP 112
FDRLVSSGY-IYDPVMREVETAFMPWLKEQAIGYLAR----
                                                                                      Conservative
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                                                                                                      5.9%;
25.6%;
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                                                                             Score 104.5; DB 3;
Pred. No. 0.074;
33; Mismatches 95;
                                                                                                                         Length 552;
  -----GVVARRVVDK 338
                                                                                    Indels
                                                                                  87;
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; LENGTH: 1939
; TYPE: PRT
; ORGANISM: HOMO s
US-09-310-187A-1
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US-08-216-894-2
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APPLICANT: Benichou, Gilles
APPLICANT: Fedoseyeva, Eugenia
APPLICANT: Fedoseyeva, Eugenia
TITLE OF INVENTION: Involvement of Autoantigens in Cardiac
TITLE OF INVENTION: Graft Rejection
                                                                                                                                              Sequence 2, Application US/08216894 Patent No. 5876734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09310187A Patent No. 6358751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/310,187A
CURRENT FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                        GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1477
                                                                                                                                                                                                                                                                                                                                                                                   1581 KDEEMEQAKRNHQRVVDSLQTSLDAETRSRNEVLRVKKKMEGDLNEMEIQLSHANRMAAE 1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1528 LEKVRK----QLEVEKLELQSALEE---AEASLEHEEGKILRAQLEFNQIKAEIERKLAE 1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1422
                                                                                                                                                                                                                                                                                     1641 ---- AQKQVKSLQSLLKDT 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 TTMRSELGKLS------XDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 LRYEIKDIHVPPRVKESMQMQVEAERRKRATVLE-----SEGTRESAINVAEGKKQAQ 225
                                                                                                                                                                                                                                                                                                                                                                                                                                  233 KAEQINQAAGEASAVL-----AKAKAKAEAIRI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 PPRVKESMOMOVEAERRKRATVLESEGTRESAINVAEGK------KQAQILASEAE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 VSAFSKLAKDSNTILLPS--NPGDVTSMVAQAMGVYGALTKAPVPGTPD 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 EAANAKWEADKAEAAEKARAEAEAAAEEQKALLEELAATAAAEAEERGEEPPAEPPS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 RYVQSLKEIVINVPEQ--SAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQ 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILAS---EAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQY 282
                                                                                                                                                                                                                                                                                                                                    SLTVAEQYVSAFSKLAKDS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSLSTELFKLKNAYEESLEHLETFKRENKNLQEEISDLTEQLGEGG------KNVHE 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLQNEIEDLMVDVERSNAAAALDKKQRNFD--,---KILAEWKQKYEESQSELESSQKEA 1476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54;
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                                                                                                                                                                                                                                                                                                                                                                                                                             -LAAALTQHNGDAAA 274
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TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-216-894-2
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Search completed: September 22, 2002, 18:21:40 Job time: 3406 sec
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MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//8/216/894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELLEPHONE: (202)672-5300
TELEPHONE: (202)672-5399
TELEFAX: (201)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.6%; Score 99.5; DB 2; Length 564; Best Local Similarity 23.5%; Pred. No. 0.24; Matches 50; Conservative 42; Mismatches 80; Indels 41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley 6 Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                 321 ETAKTDEVEKORAAEAAKAVETEKORAAEATKVAEAEK-RKAAEAAKAVETEKORAAEAT 379
                                                                                                                                                                                                                                                                                                                                           113 YKASYGVED------PEYAVTQLAQ-----TTMRSELGKLSXDKVFRERESLNASIVD 159
                                                                                                                       380 KV-AEAEKQKAAEAAKAVETEKQRAAEATKVAE 411
                                                                                                                                                                                                                                                             200 KRATVLESEGTRES-AINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAI 258
                                                                                                                                                                                                                                                                                                               261 AINRATKLEEERNQAYKAAHKAEEEKAKTFQRLITFESENINLKKRPNDAVSNRDKKKNS 320
                                                                                                                                                                                                                                                                                                                                                                                               206 WOATFGGGDHPPKSDLVPRGSPSQLQQAENNITNSKKEMTKLREKVKKAEKEKL-----D 260
                                                                                                                                                                    259 RILAAALTOHNGDAAASLTVAEQYVSAFSKLAK 291
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ZIP: 20007-5109
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Result
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length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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356
378
378
3007
3019
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                  PCT-US98-12125-145

16 US-09-209-462B-150

16 PCT-US01-03800A-2351

1 PCT-US01-04098A-3196

1 PCT-US01-04942A-222

1 PCT-US01-08656-10594
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    PCT-US01-04098A-1228
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Sequence 145, App
Sequence 150, App
Sequence 3319, Ap
Sequence 3196, Ap
Sequence 222, App
Sequence 10594, Ap
Sequence 1228, Ap
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-09-902-540-1133	-09-803-110-1151	-09-739-449-115	-60-215-161-7262	-09-897-516-726	-489-039A-132	-09-543-681A-6978	-60-096-409-1685	-09	-09-708-427-1254	S-09-620-394B-403	-09-708-427-5709	9-417-507-3256	-60-324-109-3211	9-806-866-1	-09-806-866-1	-09-806-866-1	-09-806-866-1	-806-866-13	-09-708-427-5	-09-708-427-5709	-09-767-129-2	-09-395-397-2	-09-708-427-5669	-09-708-427-	-09-708-427-5669	S-09-708-427-1254	S-09-620-394B-403	S-60-167-217-552	-US01-04942A-59	-191-637-543	S-09-614-150-541	S-09-724-497-3	S-09-723-594-3	S-09-298-733A-	S-09-298-733-36	S-09-209-462B-4	US98-12125-27
equence 1133	equence 1151	equence 11515,	nce 7262,	e 7262,	e 13296,	ce 6978,	зе 16859,	Sequence 16859, A	e 12543,	e 4031,	e 5709	e 325	зе 3211	Эе 11,	ă	ŭ	й	ö	ĕ	ď	ĕ	ö	á	e 56696,	ĕ	ĕ	9	ë	ŧυ	equence 5433	equence 5415, A	equence 36	ce 36,	equence 36, A	equence 36, Ap	quence 4	Sequence 272, App

ALIGNMENTS

RESULT 1 PCT-US98-12125-145

Sequence 145, Application PC/TUS9812125 GENERAL INFORMATION: APPLICANT: Rosen et al.

Rosen et al.

WENTION: 86 Human Secreted Proteins
SEQUENCES: 318

TITLE OF INVENTION: 86
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

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ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPB: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION NUMBER: PCT/US98/12125
FILING DATE: Jan 01, 1900
CLASSIFICATION:
APPLICATION NUMBER: PCT/US98/12125
FILING DATE: Jan 01, 1900
CLASSIFICATION NUMBER: PTICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: ATTORNEY/AGENT INFORMATION:
NAME: A. Anders BTOOKES
REGISTRATION NUMBER: PZ008Complete
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/209,462B
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TITLE OF INVENTION: 86 Human Secreted Proteins
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TOPOLOGY: 11077
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LENGTH: 356 amino acid
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les 341; Conservative
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R APPLICATION NUMBER: 60/04
R FILING DATE: 1997-06-13
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OR FILING DATE: 1997-06-13
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Pred. No. 3.7e-143;
2; Mismatches 11;
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PRIOR TILING DATE: 1997-10-02
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             299 PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS 356
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OR APPLICATION NUMBER: 60/05
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FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/058,975
FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/060,834
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FILING DATE: 1997-10-02
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FILING DATE: 1997-08-18
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                                                                                                                                                                          QAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILL 298
                                                                                                                                   DIHVPPRVKESMOMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN 238
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PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASLDEELDRVKMS
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Pred. No. 3.7e-143;
2; Mismatches 11;
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             PRIOR APPLICATION NUMBER: Not Yet Assigned PRIOR APPLICATION UMBER: 09/728, 422
PRIOR APPLICATION UMBER: 09/728, 422
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/663,561
PRIOR APPLICATION NUMBER: 09/664,936
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR APPLICATION NUMBER: 09/620,325
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PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: CUStom
SEQ ID NO 2351
LENGTH: 378
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Best Local Similarity
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APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: PCT/US01/04098A CURRENT FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Novel Nucleic Acids and FILE REFERENCE: 21272-029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/620,325 FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAAGEASAVLAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILL 320
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                                                                                                                                                                                                                                                           2001-02-05
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Pred. No. 4.1e-143;
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; ORGANISM: Homo sapiens PCT-US01-04942A-222
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                                     SEQ ID NO 222
LENGTH: 3007
TYPE: PRT
                                                                                                             PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19
PRIOR PPLICATION NUMBER: 09/616,847
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 222, Application GENERAL INFORMATION:
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SOFTWARE: Custom
SEQ ID NO 3196
SEQ ID NO 3196
TURNETH: 378
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides FILE REFERENCE: 21272-045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
                                                                                                                                                                                                                                                                                                              PRIOR EILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: PCT/US01/04942A CURRENT FILING DATE: 2001-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-06-20 PRIOR APPLICATION NUMBER: 09/560,875
                                                                                                NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hyseq,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIHVPPRVKESMOMQVEAERRKRATVLESEGTRESAINVAEGKKOAQILASEAEKAEQIN 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIK 178
                                                                                                SEQ ID NOS:
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Pred. No. 4.1e-143;
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CURRENT APPLICATION NUMBER: PCT/US01/08656
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
SOFTMARE: CUSTOM
SEQ ID NO 10594
LENGTH: 3019
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PCT-US01-08656-10594
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Best Local S
Matches 340
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APPLICANT: HYSEG, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC
FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10594,
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                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(3019)
OTHER INFORMATION: Xaa = X or *
-US01-08656-10594
                                                                                                                                                                                                                                          NAME/KEY: DOMAIN
LOCATION: (2426)..(2903)
COTHER INFORMATION: ATPases associated with various cellular act domain OTHER INFORMATION: identified by PFam, accession name AAA, E-value-3.3, OTHER INFORMATION: score of 618.7
                                                                                                                                                                                                                                                                                                                                NAME/KEY: DOMAIN
LOCATION: (115)..(144)
OTHER INFORMATION: accession number BL01270C, p-value-6.745e-17, raw score of 16.91
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                 LEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYG
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Similarity
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                                                                                                              Conservative
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                                                                                                             Score 1643; DB 1; Length 3019;
Pred. No. 2e-141;
3; Mismatches 11; Indels 4
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PCT-US01-04098A-1228
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PRIOR APPLICATION NUMBER: 09/663,561
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR PPLICATION NUMBER: 09/620,325
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/560,875
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Custom
SEQ ID NO 1228
LENGTH: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1228, Application PC/TUS0104098A GENERAL INFORMATION:
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                        Matches 341;
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 3960
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PRIOR APPLICATION NUMBER: 09728,422
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/693,325
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VEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIK 178
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DIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN
                                                                                                                                                                    LEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYG
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                                             VEDPEYAVTQLAQTTMRSELGKLSLDKVFRERESLNASIVDAINQAADCWGIRCLRYEIK
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PCT-US98-12125-272
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TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PZ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TITLE OF INVENTION: 86 Human Secreted Proteins
NUMBER OF SEQUENCES: 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239
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OPERATING SYSTEM: MSDOS version 6.2
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                                                                                                                                                                                                                        51 RMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIM 110
                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                              PSNPGDVTSMVAQAMGVYGALTKA--PVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS 356
                                                                                     KDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEEL 350
                                            AEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLA 290
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                             AEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLA
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9410 Key West Avenue
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Pred. No. 4.3e-129;
0; Mismatches 2;
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US-09-209-462B-411
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PRIOR FILING DATE: 1997-06-13
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PRIOR FILING DATE: 1997-06-13
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FILING DATE: 1997-09-12
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FILING DATE: 1997-06-13
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FILING DATE: 1997-10-02
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FILING DATE: 1997-09-12
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APPLICATION NUMBER:
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ROSEN ET AL.
PROTION: 86 Human Secreted Proteins
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1997-06-13
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60/061,059
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PRIOR APPLICATION NUMBER: 60/061,060
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 737
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 411
LENGTH: 306
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                         CURRENT APPLICATION NUMBER: US/09/298,733
CURRENT FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: 60/082,961
EARLIER FILING DATE: 1998-04-24
EARLIER FILING DATE: 1998-05-22
EARLIER FILING DATE: 1998-05-22
EARLIER FILING DATE: 1998-06-11
EARLIER FILING DATE: 1998-06-11
EARLIER FILING DATE: 1998-06-12
EARLIER APPLICATION NUMBER: 60/091,163
EARLIER APPLICATION NUMBER: 60/091,619
EARLIER APPLICATION NUMBER: 60/091,619
EARLIER FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hoffman, Heidi
APPLICANT: Hall, Jeff
APPLICANT: Rapiejko, Peter
APPLICANT: Adams, R. Mark
APPLICANT: Agostino, Michael J.
APPLICANT: Fechtel, Kim
APPLICANT: Howes, Steve H.
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  NUMBER OF SEQ ID NOS: 79
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36
LENGTH: 305
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Best Local Similarity 99.3%;
Matches 304; Conservative
                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Secreted Proteins and TITLE OF INVENTION: Encoding Them FILE REFERENCE: AG199-02pM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Valenzuela, Dario APPLICANT: Yuan, Olive
TYPE: PRI
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Pred. No. 4.3e-129;
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; SEQ ID NO 36;
; LENCTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-298-733A-36
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TITLE OF INVENTION: Secreted Proteins and Polynucleotides
TITLE OF INVENTION: Encoding Them
FILE REFERENCE: 1966.1009-000
CURRENT APPLICATION NUMBER: US/09/298,733A
CURRENT FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: 60/082,961
PRIOR FILING DATE: 1998-04-24
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/086,402
PRIOR APPLICATION NUMBER: 60/086,904
PRIOR APPLICATION NUMBER: 60/088,994
PRIOR APPLICATION NUMBER: 60/089,163
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,619
PRIOR APPLICATION NUMBER: 60/091,619
PRIOR APPLICATION NUMBER: 60/091,619
PRIOR APPLICATION NUMBER: 60/091,619
PRIOR APPLICATION NUMBER: 60/091,619
PRIOR APPLICATION NUMBER: 60/091,619
PRIOR FILING DATE: 1998-07-02
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GENERAL INFORMATION:
APPLICANT: Valenzuela, Dario
APPLICANT: Yuan, Olive
APPLICANT: Hoffmann, Heidi
APPLICANT: Hall, Jeff
APPLICANT: Rapiejko, Peter
                                                                      Query Match 84.3
Best Local Similarity 99.3
Matches 303; Conservative
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Best Local Similarity 99.3%;
Matches 303; Conservative
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo
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MGREHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMD 111
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                                                                                                                                                                                                                                                            FastSEQ for Windows Version
                                                                                         84.2%;
99.3%;
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                                                                      Score 1488; DB 16;
Pred. No. 1.2e-128;
0; Mismatches 2;
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Pred. No. 1.2e-128;
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CURRENT FILING DATE: 105/09/723,594
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/298,733
PRIOR FILING DATE: 1999-04-23
PRIOR PELING DATE: 1999-04-24
PRIOR PELING DATE: 1999-04-24
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/086,402
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/088,994
PRIOR APPLICATION NUMBER: 60/089,163
PRIOR APPLICATION NUMBER: 60/089,163
PRIOR APPLICATION NUMBER: 60/089,163
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US-09-723-594-36
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US-09-723-594-36
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GENERAL I
                                                                                                                                                        Query Match
Best Local Similarity
Matches 303; Conserv
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APPLICANT: Yuan, Olive
APPLICANT: Hoffmann, Heidi
APPLICANT: Hall, Jeff
APPLICANT: Hall, Jeff
APPLICANT: Rapiejko, Peter
ITTLE OF INVENTION: Secreted Proteins and Polynucleotides
TITLE OF INVENTION: Encoding Them
FILE REFERENCE: 1966.1009-002
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e 36, Application US/09723594 INFORMATION:
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                                                                                                                                                     84.2%; Score 1488; DB 21; 99.3%; Pred. No. 1.2e-128; tive 0; Mismatches 2;
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                                                                                                                                                                               Length
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APPLICANT: MALL, DELA
APPLICANT: Applejko, Peter
TITLE OF INVENTION: Secreted Proteins and Potential Proteins and Potential Proteins and Potential Proteins and Potential Proteins and Potential Proteins and Potential Proteins and Potential Proteins and Potential Proteins application Number: US/09/724,497; CURRENT FILING DATE: 2000-11-28; PRIOR APPLICATION NUMBER: 09/298,733; PRIOR FILING DATE: 1990-04-23; PRIOR FILING DATE: 1998-04-24; PRIOR FILING DATE: 1998-05-22; PRIOR APPLICATION NUMBER: 60/086,402; PRIOR FILING DATE: 1998-06-01; PRIOR FILING DATE: 1998-06-01; PRIOR APPLICATION NUMBER: 60/089,163; PRIOR APPLICATION NUMBER: 60/089,163; PRIOR APPLICATION NUMBER: 60/091,619; PRIOR FILING DATE: 1998-06-12; PRIOR APPLICATION NUMBER: 60/091,619; PRIOR FILING DATE: 1998-07-02; NUMBER OF SEQ ID NOS: 79; SOFTWARE: FASTSEQ for Windows Version 3.0; SEQ ID NO 36; LENGTH: 305
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                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                     292 DSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELD
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                                                                                                                             EKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAK 291
                                                                                                                                                                                      CLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEA
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RVKMS
                                     DSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASLDEELD
                                                                                                              EKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAK
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Hall, Jeff
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1488; DB 21; Pred. No. 1.2e-128;
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301 RVKMS

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CURRENT APPLICATION NUMBER: US/09/614,150
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/164,932
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/184,831
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US-09-614-150-5415
                   RESULT 15
US-60-191-637-5433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5415
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Best Local Similarity
Matches 209; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Sequence 5433, Application US/60191637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DETECTION KIT, SUCH AS TITLE OF INVENTION: ARRAYS, FOR DETECTING TITLE OF INVENTION: DROSOPHILA GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Venter, J. Craig APPLICANT: et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-03-23
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                                                                                                                                                                                                                                          EGKRKSRILASEAERQEHINKASGEAAAIIAVADARARSLLAIAKSLSHLDGQNAASLTL 240
                                                                                                                                                                                                                                                               EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTV 278
                                                                                            VKGVGACLNAKSVEYKELQEDKSSVKMN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Search completed: September 22, Job time: 728 sec

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APPLICANT: Venter, J. Craig
TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO00392
CURRENT APPLICATION NUMBER: US/60/191,637
CURRENT APPLICATION NUMBER: US/60/191,637
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 42660
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: PATEROCOURTER
OF COLUMN DESCRIPTION
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Best Local
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                                                                                                              LQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIV 158
                            VQGTDA-----SXDEELDRVKMS 356
VKGVGACLNAKSVEYKELQEDKSSVKMN
                                                        AEQYIGAFKKLAKTNNTMILPSNPGDVNGFVAQALAVYNHVSNS----
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                              ; Score 1064.5; DB 26; Pred. No. 2.1e-89; 55; Mismatches 47;
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